Perfect score:

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Database

Arabidops

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AF360201 Arabidops
AB049069 Arabidops
AF428375 Arabidops
AY057578 Arabidops
AY045843 Arabidops
AY065268 Arabidops
AP065263 Oryza sat
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AB010073 Arabidops
AB01235 Arabidops
AB019235 Arabidops
AB2384 Sequence 9
AJ010829 Triticum
AL022141 Arabidops
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AB028185 Oryza sat
ACO11698 Arabidops
ACO16829 Arabidops
ACO77035 Arabidops
ACO12394 Arabidops
ACO12395 Arabidops
ACO16835 Streptoca
AVOG1835 Streptoca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Spermatophyta;
Epermatophyta; Magnoliophyta; endicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
I (bases 1 to 1272)
Xie,Q., Frugis,G., Colgan,D. and Chua,N.H.
Arabidopsis NACI transduces auxin signal downstream of TIRI to promote lateral root development
Genes Dev. 14 (23), 3024-3036 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (24-ocr-1999) Plant Cell Biology, Institute of Molecular Agrobiology, 1 Research Link, The National University of Singapore
                                                                                                      P.hybrida m
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AB012243 Arabidops
AC005310 Arabidops
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AP000388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AF198054 11near 1272 bp mRNA linear Arabidopsis thaliana NAC1 (NAC1) mRNA, complete cds AF198054.1 GI:6649235
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AB028185
ATAC011698
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OSJN00003
AC027035
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AF428375
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Xie,Q. and Chua,N.H.
Direct Submission
98.8 1272
66.5 96489
26.5 10320
21.6 1206
13.7 1188
13.0 81020
12.2 1471
12.1 1307
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TITLE
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                                                                     July 15, 2002, 06:40:44; Search time 1825.85 Seconds
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      GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                            1797656 seqs, 10463268293 residues
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                                                 nucleic search, using sw model
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Maximum Match 100%
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EDWVLCRVFHKNTEGVICRDNMGSGFDETAGASLPPLAMDPYINFDQEPSSYLSDDHHY
INBHYPGFSNLSQNOTLNSNLTNSVJELKIPCKNPNPLFTGGSASATLTGLDSFCSS
DQWVLRALLFQTHX IDGSLGPFRSQSYGEGSSESLLTDIGIPSTVWNC"

303 c 268 9 320 t
                                                                                                                                                                    /translation="METEEEMKESSISMVEAKLPPGFRFHPKDDELVCDYLMRRSLHN
NHRPPLVLIQVDLNKCEPWDIPKMACYGGKDWYFYSQRDRKYATGLRTNRATATGYWK
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                                                                                                                   /note="similar to NAM, CUC2 and NAP; NAC family"
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                          /organism="Arabidopsis thaliana"
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                                                                                                                                      /product="NAC1"
/protein_id="AAF21437.1"
/db_xref="G1:6649236"
                               /cultivar="Landsberg"
/db_xref="taxon:3702"
/chromosome="1"
      Location/Qualifiers
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                                                                                                                              /codon_start=1
                                                                                     /gene="NAC1"
89. .1063
                                                                                                          /gene="NAC1"
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117604, Singapore
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Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; Core eudicots: Spermatophyta; Magnollophyta; eudicotyledons; Core eudicots: Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 96489)
Federspiel, N.A., Palm, C.J., Conway A.B., Conn, L., Hansen, N.F., Altafi, H., Nguyen, M., Lam, B., Buehler, E., Dunn, P., Gonzalez, A., Kremenetskaia, I., Kim, C., Lenz, C., Li, J., Liu, S., Luros, S., Schwartz, J., Shinn, P., Toriumi, M., Vysotskaia, V.S., Walker, M., Uupublished
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Federspiel, N.A., Palm, C.J., Conway, A.B., Conn, L., Hansen, N.F., Altafi, H., Araujo, R., Huizar, L., Rowley, D., Buehler, E., Dunn, P., Gonzalez, A., Kremenetskaia, I., Kim, C., Lenz, C., Li, J., Liu, S., Luros, S., Schwartz, J., Shinn, P., Toriumi, M., Vyotskaia, V., Walker, M., Yu, G., Ecker, J., Theologis, A. and Davis, R.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         taccacttatgacgctagacatacatatatttcatcgtagttccatttgtttcaaaaaaa 1260
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Arabidopsis thaliana chromosome I BAC T6H22 genomic sequence,
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join(15883. 15949,16151. 16337,16412. 16483,16565. 16636, 1687. 16948,1713. 17184,17313. 17384,17854. 17925, 18077. 181484,18446. 18511,18783. 18844,18955. 19331, 19631. 19829,19908. 20066,20165. 20283,20388. 20598, 20680. 20911,29992. 21142,21215. 21550)
                                                                                                                                                                                                                                                                                                                                                                                                                              QVLDACLINADDMRLYGTTFDYSYCGRONLFYCLYWLYTKLSPRKWGESGGSSTALAAL
LGGVSYLLSQEIDVRPNLAVILGLAYLDSVFLGGTCLAQVSCYWPPHRRITYVHEAGH
LLGAYLMGCPFRGYLLDPVVAMQMGVQGOAGTQFWDQKMESETABGRLSGSSFDRYSM
VLFAGTAAEALVYGEAEGENDENLFRSISVLLEPPLSVAQMSNQARWSVLQSYNLLK
WHKAAHRAAVEALQVGSPLSIVIRRIEEAMSSSK"
COMPLEMENT (4058. .4471)
   NDAFGTAHRAHASTEGVTKFLKPSVAGFLLQKELDYLVGAVSNPKRPFAAIVGGSKVS
SKIGVIESLLEKCDILLLGGGMIFTFYKAQGLSVGSSLVEEDKL"
                                                                                                                                                                                                                                                                                                                                                                   /translation="MALSPSSPPCLRSLSPSFSRQIGFLVPRVQSLVFGSVRKHELRR
PSALREWREYEDAVKRKDLAGALRFLKSIENDEQRDSVESIVTAKLSGLGALELERDW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /protein_id="aaF02832.1"

A_xxef="G1:605638"

/translation="MDEIEHTPERNHTLPLARIKKIMKADEDVRMISAEAPVIFAKA
CEMFILELTLRAWIHTEBNKRRTLQKNNIAAAISRTDVFDFLVDIIPRDELKEEGGGV
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DNDRIKNWWHTKKRLPSSSSSSLSSTHQQSFYADHOKNOGAQDEIHGGLMSGONS
AUSSHHQGECHHTREPELHEVNGLINELQFLLDHDDFDDITSEFLQDNDILFPLDSELLHN
HQTHISTQEMTREVTKSQSFDHPQPDIPCGFEDTNEESDLRRQLVESTTPNNEYDEWF
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VYVGHEMERFVVNAELLNHPVFVALLKQSAQEYGYEQQGVLRIPCHVLVFERILESLR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Putative transcription factor; putative transcription factor. MYB72,R2R3-MYB factor family member.gi|3941502"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hap5b, gi|2398532. Highly similar to CCAAT binding transcription factor from many species. The C (reverse complement) at position 4078 is a T in the cDNA sequence. gi|2398532. This puts a termination codon 4 amino acids sooner in the cDNA predicted sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="transcription factor hap5b; transcription factor
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complement(6331. .7391)
/genea"TGH22.4"

/genea"TGH22.4"
/genea"TGH22.4"
                                                                                                                                     .2690,2774. .2850,2968. .3044,
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                                                                                                                                                                                                                                        /note="Hypothetical protein"
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/gene="T6H22.5"
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/db_xref="GI:6056369"
                                                                                                                Join(1728. .2082,2382. .. 3126. .3258,3377. .3532) /gene="T6H22.2"
                                                                                                                                                                                                                                                                                                /protein_id="AAF02831.1"
/db_xref="G1:6056367"
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/db_xref="G1:6056370"
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/gene="T6H22.3"
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                                                                      1728. .3532
/gene="T6H22.2"
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/gene="T6H22.7"
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He mail for correspondence: arabésequence.stanford.edu Genes with similarity to proteins in the databases are described as 'putative', '-1ike' or 'similar to'. Genes that have EST similarity but no significant protein similarity are described as 'unknown proteins'. Genes that are annotated based only on gene prediction software are described as 'hypothetical proteins'. The software programs used to predict genes include: Grail (Informatics Group, Oak Ridge National Laboratory, Chris Burge, http://gnomic.stanford.edu/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               http://genomic.sanger.ac.uk/), and NetPlantGene (S.M. Hebsgaard, et
al., CBS, Technical University of
Denmark,http://www.cbs.dtu.dk/NetPlantGene.html).
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SAVVDSRFSVHVASKVHSVRGKGARGVITMAKKSVGDLNSVDLKGKKVFVRADLNVPL
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GIEVVKADDCIGPEVETLVASLPEGGVLLLENVRFYKEEEKNEPDFAKKLASLADLYV
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Altafi, H., Araijo, R., Huizar, L., Rowley, D., Brooks, S., Buehler, E.,
Chao, Q., Dunn, P., Gonzalez, A., Khan, S., Kremenetskaia, I., Kim, C.,
Lenz, C., Li, J., Liu, S., Luros, S., Schwartz, J., Shinn, P.,
Toriumi, M., Vyotskaia, V., Yu, G., Ecker, J., Theologis, A. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (18-OCT-1999) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304,
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                                                               Stanford University, 855 California Avenue, Palo Alto, CA 94304,
                                                                                                                                                                                                                                                                                                                                                                                                         Stanford University, 855 California Avenue, Palo Alto, CA 94304,
                                   Submitted (04-SEP-1999) DNA Sequencing and Technology Center
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/db_xref="taxon:3702"
/chromosome="I"
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/db_xref="G1:6056366"
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                                           SSGLSGEIPSSFANFVNLEEAWINDIRLTGQIPDFIGNWTKLTTLVLRNNNLTGTIPS
NGDYLGLKGRULDLSFNKLLTGOIPDFIGNSRQLTLADVSYNDLTGDLESWYRLFNLQLA
LPRLDCLQROPFRCNRGKGYVENFYNCGGEDIRSSGALYEKDEGALGPATFYSKTO
RWAVSNVGLFTGSNNRQYIALSATQFANTSDSELFQSARLSASSLARYGLGLENGGYS
RWAVSNVGLFTGSNNRQYIALSATQFANTSDSELFQSARLSASSLARYGLGLENGGYS
                                                                                                                                                                          GCCIEGNQRMLVYEYLSNKSLDQALFBEKSLQLGWSQRFEICLGVAKGLAYMHEESNP
RIVHRDVKASNILLDSDLVPKLSDFGLAKLYDDKKTHISTRVAGTIGYLSPEYVMLGH
LEKTOVFRAGTIVALEIVSGRRNSSPELDDOKQYLLEWAWSLHGEQRDWEVVDPDLTE
FDKEEVKRYAGTOVALGIVGTDHAIRPTWSRVGMLTGDVEITEANAKFGYVSERTFENA
MSFMSGSTSSSWILPFTPKDSSKSQVBEHGRRH"
22050. .28067
                                                                                                           VTVOPAEIOIOGSNTWÄSLGRRIFDIYVOGKLVEKDFDWQKAANGSSIRVIORVYKAN
VSRYLLEWHLEWAGKCTCIPAGGTYGFLVSALSATPDFITYNKNKLDSKSKRNIVII
VGAIVGAGMLCILVIAILLFRRKRKRAADEEVLNSLHIRPYTFSYSELRTATODFDP
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LVXISNLNLNQNFLTGPLSPGIGNLTRMQWIAIDMNNFSGSLPPEIGNCTRLVKMYIG
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Pred. No. 1.2e-214;
0; Mismatches 6;
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Best Local Similarity 90.0°
Matches 972; Conservative
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Sukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                       tactattgctatattcctatccatgattggaacaattcttcggggggaaataacgtgtgc
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82584 CAGTGATCATCACTACATCATCAATGAGCACGTACCCTGCTTCTCCCAATTTGTCACA
                                                                                                      gaaccaaaccttaaactcgaacctaaccaactcagtctctgaactcaagattccatgcaa
                                                                                                                                                                                                                                                                                                         844 gaaccctaaccccttgtttactggtggttcagcctcagccacgctcacaggcctcgactc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tggaagcctcgggcctaaagaatcacagagttatggagaaggtagctcggagagcctcct
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2 (bases 1 to 106320)
Ecker,J.R.
Direct Submission
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Direct Submission
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complement(join(2385, .2501,2665, .2763,2933, .3227,
3290, .3928,3985, .4183,4476, .4630,5451, .6164,6220, .6499,
6648, .6823,6906, .6974,7167, .7221,7728, .8031))
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TNQRLYVIFLISTYTFTINGKLKKKKFFFAPRI
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KSMKKAMKIASAKPGVRSVSIQGQNDQLVLLGEGIDLAELTRELKKKVCMTTIITVQA
APPQQPPQPHPMGGYNQMPPARRCTCEIPNSGFCGFCRSMSQPNYQVVPSPYYPPMLY
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FNFPHTGFHRKESDPCQIQPAAATLRNLFKDFLHGASHMLRADGEVHYSHKNKAPFCY
WNLEELASRCFLYLIQLEAFEKRNYPGYENKRGDGSRCDQPFLLGECSTFKFRFSRVA
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LQRMVIRTRPHHYTKESSETRRLLCQDYAVQASQEPFPERSLRFRGVSHGIHNGRVR
KMLIRNSTGESRKLRMRRQRNLKIRDSDGDEEVWVKHYSSNHQILLVVGEGDFSFSHSL
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GFFNGASRLLRANGEVHVSHKNKAPFSEWNLEELASRCFLVLIQRVAFEKNNYPGYEN
KRGDGRRCDQPFLLGECSTFKFRFSRVAKELYAEKVRSREVKERESMYPEAILNKQPV
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                                                                                                                                                                                                                                             Submitted (13-MAY-2000) Arabidopsis thaliana Genome Center, Submitted (13-MAY-2000) Arabidopsis thaliana Genome Center, Department of Biology, University of Pennsylvania, 38th Street and Hamilton Walk, Philadelphia, Pennsylvania 19104-6018, USA (bases 1 to 106320)
Cheuk, R., Shinn, P., Brooks, S., Buehler, E., Chao, O., Choin, C., Klan, S., Kim, C., Altafi, H., Bel, B., Chin, C., Chiou, J., Choi, E., Conn, L., Conway, A., Gonzalez, A., Hansen, N., Howing, B., Koo, T., Lam, B., Lee, J., Lenz, C., Li, J., Liu, A., Liu, J., Schwartz, J., Southwick, A., Thaveri, A., Toriumi, M., Vaysberg, M., Vu, G., Davis, R., Federspiel, N., Theologis, A. and Ecker, J. Direct Submission
                           Submitted (14-APR-2000) Arabidopsis thaliana Genome Center, pepartment of Biology, University of Pennsylvania, 38th Street and Hamilton Walk, Philadelphia, Pennsylvania 19104-6018, USA (bases 1 to 106320)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (28-JUN-2000) Arabidopsis thaliana Genome Center, Submitted (28-JUN-2000) University of Pennsylvania, 38th and Hamilton Walk, Philadelphia, PA 19104-6018, USA On May 13, 2000 this sequence version replaced gi:7549540. Location/Oualifiers
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join(455. .553,875. .1189)
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Direct Submission
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JOURNAL
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join[12990. .13164,13696. .13745,13837. .13912,13998. .14118, 14217. .14320,14419. .14740,14908. .15157,15251. .15628, 1578. .16611)
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TFGSFDSNFVKEVSSSNGASGGYDSNFESSHGTGDDBRESSPTTNGTTGVAARFYTE
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AYGORARLSVFGLYPGLSAIGQPVNTEAAETQPGNSNSPPISLYSTPPDQSSTAAATQ
QTNFLRQQYPPNFFPYGYXSPYXMPPPYIHQFLSPNGIPDGSSFPQGAALTAPSHAKP
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VNPMYNIAYGQPLGFPVQAQAIGGLMGMHQPTQPMAASTTYQTLPPPPHTTTAMGE
PIGHPHIAYQOPQAALTNWVNNY"
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LQNQHDVLLEELESGSSQLCSLESELELLQMAAERLLDDKKPGGSYLEQLNOQLVVKR
CNIMDLKKQMYEQYYIYFKLKASMHSVSWTTSGHDGRVMYRMITKYIMSSFRDDVRLT
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FNDPHETAQKLLFLDTFHEVRSKREKKKEASPIVPVTQPSGRGGRRNFASSNSYQGSS
GRNASFKRENGANHVTRGSRTAQPATNKASNITVPNETKVSGPASIPSEVSNHKAQDD
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CDSPLVFFTLRSGLGGFSYLCENHAETDCMCCLRQFLHPSEDDSYRLVRFLVERLSEI
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DHPDAFDTEQLLSSMEKLRKGQAVDIPNYDFKSYKNNVFPPRRVNPSDVIILEGILIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SERHVLLLDPILGTAGNSAVQAIRLLISKGVPESNIIFLNLISAPEGVNVVCKKFPRI
KIVTSEIELGLNDEFRVVPGMGEFGDRXFGTDDE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(join(16511. 16739,16880. 17104,17226. 17722, 17878. 18357,18375. 18440,18538. 18798))
/note="hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEGRKTLTAGDIASRPKMETFRDISDDMMVNEDKDETFDMHIQKVEAVLKDLTMTSEK
SFDHRYRLQTEFEGVSQRPVLFDLSYRGDYNLRQVQDPLVKSRERTSPLDLCYYQERR
                                                                  SFPHLYAGESPERHRILGODFPVQASOEPLSEYSNRWSGVSREIYNWEVTYLRKNFSG
YGDGNKVSEAWSDSSISKNGVIYEIIIFVAVLLEDHFSVNDSLEDITWTRGLDNLQIS
                                       CLQLEDSRYSERSSLLSQDFPFQTNHHRQEQFHESSTRRTRVSPDIYDE1IQRMLTRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  join(9866. 10019,10085. 10176,10278. 10347,10460. 105
10791. 10974,11021. 11100,11177. 11371,11464. 11547,
11621. 11741,11789. 11849,11919. 12181,12242. 12327,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12447. .12596)
/note="unknown protein; similar to ESTs gb|T46383.1, gb|N96614.1, gb|A1730005.1, and gb|A1996700.1"
/codon_start=1
                                                                                                                                                                                            join(8720. .8773,9069. .9338)
                                                                                                                                                                                                                            /note="hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /evidence=not_experimental
/product="F14J16.7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /evidence=not_experimental
/product="F14J16.6"
/protein_id="AAF79311.1"
/db_xref="G1:8778302"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /evidence=not_experimental
/product="F14J16.5"
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/protein_id="AAF79310.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=1
                                                                                                                                                                                                                                                                       /codon_start=1
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DB '8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Phaseolus vulgaris"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SFGEGSSESYLSEVGMPHMWNNY"
                                                                                                                                                                                                                                                                                                                                                                  1206 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /cultivar="red kidney"
/db_xref="taxon:3885"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 (bases 1 to 1206)
Whitelaw, C.A. and Tucker, M.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                             AF402602
AF402602.1 GI:15148911
                                                                                                                                                                                                                                                                                                                                                                                                                                          Phaseolus vulgaris.
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Best Local Similarity
Matches 419; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Phaseolus.
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                                                                                         1024
                                                                                                                                                                                                                                                                                                                                                                                             ACCESSION
VERSION
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TITLE
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AF402602
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                                                                                                                                                                                                                                                                                                                                                                                                                           KEYWORDS
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                                                                                                                                                                                  /translation="MSITNEEAVKQLFALMEDVDDSLRESYRKSPFCDVDGGFTNACV
MLONHIGGYPTENLLEFLKARDGNVQKAHKMLLECLEWRTQNEIDKILTKPIYPVDLY
RGIRPTQLVGVSGYSKEGLPIAIGGVGLSTYRKASVHYYVQSHIQMNFYERDRVYLPSA
SKKQGRPICTCLKILDMSGLKLSALSGIKLWTAITITDLMYPERFTYYVNYPYIF
SACWKTIKPLLQERTKKKIQVLKGGGKDELLKIMDYESLPHFCRREGSGSGRHISNGT
TREVKKDPAVRQVYKLLTSIHSIFEQI;SEKILMTDRFRRETVDYEKKLGSITARGMSL
                      join(22484. .22538,22651. .22679,23019. .23159,23264. .2
23400. .23477,23580. .23633,23718. .23777,23863. .23958,
24055. .24237,24327. .24611),
/note-msimilar to polyphosphoinositide binding protein
Sship gb|AAB94598.1; similar to ESTS dbj|AV442135.1,
                                                                                                                                                                                                                                                                                                                                                96263 CGCGACGGGGCTGAGAACTAACCGAGCAACGGCCACCGGATATTGGAAAGCCACCGGCAA 96204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                96084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96023 ATCCAGTTATTGATCGTCAGTTAATCTCTTAGCAAATCTGTAACGAGTAATATACGT 95964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95843 ATCGCTTCCTCCACTGATGGATCCTTACATCAACTTTGACCAAGAACCCTCTTCTTATCT 95784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     266
                                                                                                                                                                                                                                                                                                                               286 aaaaatggcatgcgtgggaaggaaggattggtatttctacagccaaagagccgaaaata 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                  agacagaaccattctaagaaagggtaagctagttgggatgaggaagacattggttttcta 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----aggaagactgggtcttgtgtagggtattccataagaa 603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                atcgcttcctccactgatggatccttacatcaactttgaccaagaaccctcttcttatct 723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     724 cagtgatgatcatcactacatcatcaatgagcacgtaccctgcttctccaatttgtcaca 783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gaaccaaaccttaaactcgaacctaaccaactcagtctctgaactcaagattccatgcaa 843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6; Indels 102; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tcaaggtcgagctcctcgaggccgtaaaaccgattgggtcatgcacgaattccgtctcca
                                                                                                                                                                                                                                                                                                                                                                                       346 cgcgacgggctgagaactaaccgagcaacggccaccggatattggaaagccaccggcaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96143 TCAAGGTCGAGCTCCTCGAGGCCGTAAAACCGATTGGGTCATGCACGAATTCCGTCTCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               526 aggatotoatcotocoaatcattototgagototocoaa----------
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                                                                                                                                                                                                                                                                          66.5%; Score 856.4; DB 8;
                                                                                                                                                                                                                                                                                      Pred. No. 1.2e-214;
0; Mismatches 6;
                                                                                                              /codon_start=1
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/product="Fl4J16.8"
/protan_id="AAR79312.1"
/db_xref="GI:8778303"
                EKLQADLDAIRKENESLKK"
                                                                                                                                                                                                                                                                                      ilarity 90.0%;
Conservative
                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                    Matches 972;
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Abaseolus vulgaris NAC domain protein NAC1 mRNA, complete cds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /traislation="MSNISMVBAKLPPGFRFHPRDEELVCDYLMKKLTHNDSLLMIDV
DLNKCEPWDIPETACVGGKDMYFYTGRDRKYATGLÆTNRAARGSWERTGRDRPILRK
GTLVGMRKTLVFYQGRAPKRKTEWVMHEFRIEGENGPREPKYSSKEDWVCRVFYKSR
EVSAKPRAGSCVEDFJCSSSLPALMDSYISFOOTOAHADEFEGVPCFSIFSQNOANPIE
NHMTYMEPKLPATTYGGAPNLGYCLDPLSCDRKVLKAVLSQITKMERNPLNQSLKGST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Phaseolus vulgaris
Sukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta; eudicotyledons; core eudicots;
Rosidae, eurosids I; Fabales, Fabaceae, Papilionoideae, Phaseoleae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20705,
                                                                                                                                                                                                                                                                                                                                              tactattgctatattcctatccatgattggaacaattcttcgggggggaaataacgtgtgc 1143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (25-JUL-2001) Soybean Genomics and Improvement Lab,
USDA/ARS, BARC-west, 10300 Baltimore Avenue, Beltsville, MD 2
                                                                                                                                                gaccgacatcggtattccaagcactgtttggaattgctgatgatcgagtgtaacgagagt
tggaagcctcgggcctaaagaatcacagagttatggagaaggtagctcggaagacctcct
                                                                                                                                                                                                                                                              18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1206;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=1
/ppoduct="NAC domain protein NAC1"
/protein_id="AAK84883.1"
/db_xref="GI:15148912"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="leaf abscission zone"
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/evidence=experimental
/product="putative NAM protein"
/protein_id="AALO7176.1"
/db_xref="G1:18810577"
/translation="MDYEASRIVEMVEDEEHIDLPPGFRFHPTDEELITHYLKPRVFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="At5g39610"
/note="Is a member of the No apical meristem (NAM) protein
family PF02365"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TFFSATAIGEVDLNKIEPWDLPWKAKMGEKEWYFFCVRDRKYPTGLRTNRATEAGYWK
ATGKDKEIFKGKSLVGMKKTLVFYKGRAPKGVKTNWVMHEYRLEGKYCIENLPOTAKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EWVICRVEQKRADGTKVPMSMLDPHINRMEPAGLPSLMDCSQRDSFTGSSSHVTCFSD
QETEDKRLVHESKDGFGSLFYSDPLFLQDNYSLMKLLLDGQETQFSGKPFDGRDSSGT
                                                                                                                                                                                                                                                                          The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAFL cDNAs: Yamada,K., Banh,J., Banno,F., Dale,J.M., Goldanith,A.D., Lee,J.M., Onodera,C.S., Quach,H.L., Tang,C.C., Toriumi,M., Yamanura,Y., Yu,G., Yu,S., Bowser,L., Chen,H., Cheuk,R., Jones,T., Karlin-Neumann,G., Kim,C., Poseama,E., Lam,B., Lin,J., Meyers,M.C., Miranda,M., Nguyen,M., Palm,C.J., Shinn,P., Southwick,A., Tracy,S.E., Davis,R.W.,
                                                                                   Submitted (12-SEP-2001) Plant Gene Expression Center, 800 Buchanan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yamada,K. (SSP/PGEC) and Seki,M. (RIKEN GSC) contributed equally this work. Shinozaki,K. (RIKEN GSC) and Theologis,A. (SSP/PGEC) contributed equally to this work as PIs.
                                                                                                Street, Albany, CA 94710, USA
RIKEN Genomic Sciences Center (GSC) members carried out the
collection and clustering of RAFL cDNAS (RAFL CDNA: 'RIKEN
Arabidopsis Full-Length CDNA'): Seki,M., Narusaka,M., Ishida,J.,
Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J.,
Hayashizaki,Y. and Shinozaki,K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="This clone is in a modified pBluescript vector (FLC-1) as a BamHI/XhoI insert.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     78 aggatcaaatcatggagacggaagaagagatgaaggaaagtaatataagcatggtggagg 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       116 AGGATAAAATGGATTACGAGGCATCAAGAATCGTCGAAATGGTAGAAGATGAAGAACATA 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      198 tgatgagacgatcgcttcacaataatcatcgaccacctcttgtcctgatccaagtcgatc 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     233 ACCICAAACCAAAGGITITCAACACITICTICTICTGCIACTGCCAITGGTGAAGTIGAIC 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         138 caaagttgcctccgggattcagatttcacccgaaggacgatgagcttgtctgcgattact 197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1188;
Satou, M., Seki, M., Shinn, P., Southwick, A., Tracy, S.E. Shinozaki, K., Davis, R.W., Ecker, J.R. and Theologis, A. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches 204; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 176.6; DB 8;
Pred. No. 1.2e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Arabidopsis thaliana"
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/gene="At5g39610"
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yamada,K., Banh,J., Banno,F., Dale,J.M., Goldsmith,A.D., Lee,J.M., Yamada,K., Banh,J., Banno,F., Toriumi,M., Yamamura,Y., Yu,G., Yu,S., Bowser,L., Carninci,P., Chen,H., Cheuk,R., Hayashizaki,Y., Ishida,J., Jones,T., Kamiya,A., Karlin-Neumann,G., Kawai,J., Kim,C., Koesema,E., Lam,B., Lin,J., Meyers,M.C., Miranda,M., Narusaka,M., Nguyen,M., Palm,C.J., Sakurai,T., Satou,M., Seki,M., Ecker,J.R. and Theologis,A.
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2 (amadak. K. Banh, J., Banno, F., Dale, J.M., Goldsmith, A.D., Lee, J.M., Onodera, C.S., Quach, H.L., Tang, C.C., Toriumi, M., Yamamura, Y., Yu, G., Yu, S., Bowser, L., Carninci, P., Chen, H., Cheuk, R., Bayashizaki, Y., Ishida, J., Yones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Kim, C., Koesema, E., Lam, B., Lin, J., Meyers, M.C., Miranda, M., Narusaka, M., Nguyen, M., Palm, C.J., Sakurai, T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        236 cttgtcctgatccaagtcgatctcaacaagtgtgagccttgggacatcccaaaaatggca 295
                                                                                                                                                                                                                                                                                                                                        355
                                                                                                                                                                                                                                                                                                                                                                                                                                            356 ctgagaactaaccgagcaacggccaccggatattggaaagccaccggcaaagacagaacc 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   416 attoctaagaaagggtaagotagttgggatgaggaagacattggttttoctatcaaggtoga 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 373 GCACCCAAAGGGAGAAAAACTGAATGGGTCATGCATGAGTTTCGCATAGAAGGTCCCCAT 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            596 cataagaatacggaaggagttatatgtagagacaacatgggaagctgttttgatgagaca 655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          487 TACAAAAGCA---GAGAAGTTTCAGCCAAACCTAGCATGGGTAGCTGCTATGAAGACACA 543
                                                                                                                                            235
                                                                                                                                                                    133 CTTCTCATGATAGATGTTGACCTTAACAAGTGTGAACCTTGGGATATTCCTGAAACAGCA 192
                                            116 agtagtataagcatggtggaggcaaagttgcctccgggattcagatttacccgaaggac 175
                                                                   22 AGCAACATAAGCATGGATGGAGGCAAAGTTGCCACCAGGGTTCAGGTTCCATCAAGAT 81
                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana putative NAM protein (At5g39610) mRNA,
                                                                                                                                          476 getectegaggeegtaaaacegattgggteatgeacgaatteegteteeaaggateteat
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FEATURES source	377 412	437 CDS	497 CDS	557 592		PLN 19-JUL-2000 : CDS	i P1 ophyta;	s. abata,s. sixty CDS	on of	oata,S.	rch 5,	ise see Tibed in	CDS	of	ouis,	may be
tcaacaagtgtgagccttgggacatcccaaaatggcatgcgtgggaggga	atttetacagccaaagagaccgaaatacgcgacggggctgagaactaaccgagcaacgg 	378 ccaccggatattggaaagccaccggcaaagacagaaccattctaagaaagggtaagctag	ttgggatgaggaagacattggttttctatcaaggtcgagctctcgaggccgtaaaacg	attgggtcatgcacgaattccgtctccaaggatctcatcatcctccaatcattctctga	<pre>gctctccaaaggaagactgggtcttgtgtagggtattccataagaatacggaagg 612 i                                      </pre>	AB026645 Arabidopsis thaliana genomic DNA, chromosome 3, Pl clone: MGH6 AB026645.1 GI:4757401	Arabidopsis thaliana (strain:Columbia) DNA, clone_lib:Mitsui Pl clone:MRH6. Arabidopsis thaliana Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;	1 (sites) Sato,S., Nakamura,Y., Kaneko,T., Katch,T., Asamizu,E. and Tabata,S. Structural analysis of Arabidopsis thaliana chromosome 3. I. Squence features of the regions of 4,504,864 bp covered by sixty	Figure 3 and TAC clones  Note: A research : an international journal for rapid publication reports on genes and genomes. 7 (2), 131-135 (2000)	0 81020) virany., Kaneko,T., Kato,T., Asamizu,E. and Tal	Submitted (28-APR-1999) Yasukazu Nakamura, Kazusa DNA Research Institute, Department of Plant Gene Research; 1532-3, Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:ynakamu@kazusa.or.jp, rei:81-438-52-3935, Fax:81-438-52-3934)	Address for correspondence: kaos@kazisa.or.jp  For the latest information on annotation of this clone, please  http://www.kazusa.or.jp/kaos/cgi-bin/agd_graph.cgi?c-mGH6  Genes with similarity to proteins in the databases are describe 'product' or 'note' qualifiers. Genes that have no significani	arity are described as 'unknown protein'.  programs used to predict genes include: Grail proup, Oak Ridge National Laboratory,  ornl.gov/Grail-1.3/),	GENSCAN (Chris Burge, MIT, http://CCR-081.mit.edu/GENSCAN.html), NetGene2 (S.M. Hebsgaard, et al., CBS, Technical University of Denmark, http://www.cbs.dtu.dk/services/NetGene2// and SplicePredictor (Volker Brendel, Stanford University,	Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, Washington University School of Medicine, St. Louis, http://genome.wastl.edu/eddy/tRNAscan-SE Thirty-/genome.wastl.edu/eddy/tRNAscan-SE Thirty-/genome.wastl.edu/eddy/tRNAscan-SE Thirty-louis Thirty-/genome was not he the achieve incort of thir shown of the the achieve the standard the second to the standard the second the standard the second transfer of the standard transfer of the standard transfer of the standard transfer of the second t	may not be the entire insert of this clone. It
tcaacaagtgtgago             TCAACAAGATTGAGO	atttctacagccaaa                 ATTCTTCTGTGTGA	ccaccggatattggaa 	ttgggatgaggaaga                   TGGGTATGAAGAAAA	attgggtcatgcacga 	gctctccaaaggaaga            CAGCTAAGAACGA			(sites) Sato, S., Nakamura Structural analys Sequence features	DNA research : reports on qer	20277480 2 (bases 1 to 81020) Sato, S., Nakamura, Y., Direct Submission	Submitted (28- Institute, Dep Kisarazu, Chib Tel:81-438-52-	Address for co For the latest http://www.kaz Genes with sim 'product' or '	protein simila The software p (Informatics G http://compbio	GENSCAN (Chris NetGene2 (S.M. Denmark, http: SplicePredicto	Genes encoding (Sean Eddy, Wa http://genome.	This Sequence
Qy 258 Db 293	Oy 318 Db 353	Qy 378 Db 413	Qy 438 Db 473	Qy 498 Db 533	Qy 558 Db 593	RESULT 6 AB026645 LOCUS DEFINITION ACCESSION VERSION	SOURCE	REFERENCE AUTHORS TITLE	JOURNAL	MEDLINE REFERENCE AUTHORS TITLE	JOURNAL	COMMENT			•	

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                                                                                                                                                                                                                                                                                                                                                                                                                /evidence=not_experimental
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unknown protein"
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SRPOVADAIGSRENDAAEKKYGKVANGDVKPNSWTLLDFGDVVIHLFLPPQRTFYNLED
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KTQGRRIJVEAVEQGLMKTLRANDDENHIGKLNLFLEERVKSLCVENQIMRDYAQSNR
ATVNALRSNLQQVLAAVERNRWEEPPTVADDAQSCCGSNDEGDSEEERWKLAGEAQDT
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LIDNVPLRKOTSYSSYLSVCYARPSPREGAPHESTEDBOLLIXSDHPHQLNKSLISF
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24582. 24731, 44815. 25204))
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Location/Qualifiers
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CDS

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AWPETAREDLVAGFTNGSCDGDLCVGLRLGDDGAKRRRTQVTNERMRPAE"
complement (2664, 26464)
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NRSSKSTAQQPSHPPPGKDSDILESSSTSISSSRLSLSSSSPNPRLSLDLD
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ASGKIVFHGLERSSSSPGNFTGGPRMKLHHGMPRSHSANVRITPVLNVPVSSLRSGPK
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GMSGNNVHLANVPRSSEGVLSSTHFSTFSQPSQQPVEQLQVSHVNRYSMSNSGTFVSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SGLFFGQLFASSSSASSSSGNRAQLOSNNIKNRTNRSRLEPTSEL"
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                                                                                                                                                                                              DLQPSPKRQKVEKPSQFAYPDTQGNPATISAGVSQAHFSMGLQEKDRLPSDVCKPVRS
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NLYGVQTSSGSIETAVDMNSMSLNSMRRVDTSFGSQSGLQNNPLLKPHLRHQFENGNF
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Southwick, A., Karlin-Neumann, G., Nguyen, M., Lam, B., Miranda, M., Palm, C.J., Bowser, L., Jones, T., Banh, J., Carninci, P., Chen, H., Cheuk, R., Chung, M.K., Hayashizaki, Y., Ishida, J., Kamiya, A., Kawai, J., Kim, C., Lin, J., Liu, S.X., Narusaka, M., Pham, P.K., Sakano, H., Sakurai, T., Satou, M., Seki, M., Shinn, P., Yamada, K., Boker, J., Theologis, A. and Davis, R.W.
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                                                                                                                                                                                                                                                                                                                                                                                                  35192 AAGATAGAGCAATCCAAAGAAACGGTGGTCTTGTGGGTATGAGAAAGACACTTGTGTTTT 35251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            35132 ACGCAACAGGCTACAGAACAAAACGGGGTACGGCCACCGGTTATTGGAAAGCCACCGGGA 35191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     404
                                                                                                                                                                                                                                                                                                                                                                    285 caaaaatggcatgcgtgggagggaaggattggtatttctacagccaaagagaccgaaaat 344
                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     345 acgcgacggggctgagaactaaccgagcaacggccaccggatattggaaagccaccggca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                405 aagacagaaccattctaagaaagggtaagctagttgggatgaggaagacattggttttct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 465 atcaaggtcgagctcctcgaggccgtaaaaccgattgggtcatgcacgaattccgtctcc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis thaliana NAM (no apical meristem)-like protein (MEBH3.22) mRNA, complete cds.
                                                                                                                                                                                                                                                   Score 167.2; DB 8; Length 81020;
Pred. No. 3.1e-33;
0; Mismatches 58; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               e-mail for correspondence: arab@sequence.stanford.edu
                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35312 AAGGAAAACTTCTTCACCAC 35331
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ilarity 77.7%;
Conservative (
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KEYWORDS
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The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAFL cDNAs: Nguyen,M., Southwick,A., Karlin-Neumann,G., Lam,B., Miranda,M., Palm,C.J., Bowser,L., Jones,T., Banh,J., Chen,H., Cheuk,R., Chung,M.K., Kim,C., Lin,J., Liu,S.X., Pham,P.K., Sakano,H., Shinn,P., Yamada,K., Ecker,J., Theologis,A. and Davis,R.W.
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Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spenatophyta; Magnoliophyta; eudioctyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaeae; Arabidopsis.

1 (bases 1 to 1471)
Shinn, P., Chenk, R., Gholdsmith, A.D., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Lam, B., Lee, J.M., Lin, S.X., Miranda, M., Narusaka, M., Nguyen, M., Palm, C.J., Pham, P.K., Quach, H.L., Sakano, H., Sakurai, T., Satou, M., Seki, M., Southwick, A., Toriumi, M., Yamada, K., Yu, G., Shinozaki, K., Davis, R.W., Theologis, A. and Ecker, J.R.
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LYTS*
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Shinn, P., Chen, R., Kim, C.J., Banh, J., Bowser, L., Chang, M.K., Goldsmith, A.D., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Lam, B., Lee, J.M., Jones, T., Liu, S. X., Miranda, M., Narusaka, M., Nauyen, M., Palm, C.J., Pham, P.K., Quach, H.L., Sakano, H., Sakurai, T., Satou, M., Seki, M., Southwick, A., Toriumi, M., Yamada, K., Yu, G., Shinozaki, K.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (15-MAR-2001) Salk Institute Genomic Analysis Laboratory (SIGNAL), Plant Biology Laboratory, The Salk Institute for Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RATL CONAS: Shinn, P., Chen, H., Chenk, R., Kim, C.J., Koesema, E., Meyers, M.C., Tracy, S.E., Banh, J. Bowser, L., Chung, M.K., Goldsmith, A.D., Jones, T., Karlin-Neumann, G., Lam, B., Lee, J.M., Lin, J., Liu, S.X., Miranda, M., Nouyen, M., Palm, C.J., Pham, P.K., Quach, H.L., Sakano, H., Southwick, A., Tang, C.C., Toriumi, M., Yamada, K., Yu, G., Davis, R.W., Theologis, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Shinn, P. (SSP/Salk) and Seki, M. (RIKEN GSC) contributed equally to this work. Shinozaki, K. (RIKEN GSC) and Ecker, J.R. (SSP/Salk) contributed equally to this work as PIs.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 collection and clustering of RAFL CDNAS (RAFL CDNA: 'RIKEN Arabidopsis Full-Length CDNA'): Scki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.
Arabidopsis thaliana AT3g04060/T11118_17 mRNA, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RIKEN Genomic Sciences Center (GSC) members carried out the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Davis, R.W., Theologis, A. and Ecker, J.R. Direct Submission
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                                                        AF361623.1 GI:13605594
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QTDQNOGTTLNCFSSPVLNSIQADIFHRIPLYQTQSLQVSMNLQSPVLTQEHSVLHAM
IENNRRQSLKTMSVSQETGVSTDMNTDISSDFEFGKRRFDSQEDPSSSTGPVDLEPFW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CRVFQKSAGGKKIPISSLIRIGSLGTDFNPSLLPSLTDSSPYNDKTKTEPVYVPCFSN
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Southwick, A., (SSP/Stanford) and Seki, M. (RIKEN GSC) contributed equally to this work. Shinozaki, K. (RIKEN GSC) and Davis, R.W. (SSP/Stanford) contributed equally to this work as PIs. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           311 gattggtatttctacagccaaagagaccgaaaatacgcgacggggctgagaactaaccga 370
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               371 gcaacggccaccggatattggaaagccaccggcaaags.cagaaccattctaagaaagggt 430
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                491 aaaaaccgattgggtcatgcacgaattccgtctccaaggatctcatcatcctcccaatcat 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              551 tetetgagetetecaaaggaagaetgggtettgtgtgtagggtatteeataagaataeggaa 610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          131 gtggaggcaaagttgcctccgggattcagatttcacccgaaggacgatgagcttgtctgc 190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              204 CACTATCICCATAAGAAGGIICIITGACACCA---GCIITCICAGCIAAAGCIAICGGIGAA 260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   191 gattacttgatgagacgatcgcttcacaataatcatcgaccacctcttgtcctgatccaa
                                                                                                                                                                                                                                                                                                                                                                                                                                /product-"NAM (no apical meristem)-like protein"
/protein_id="AAK96835.1"
/db_xref="GI:15451128"
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                                                                                                                                         /organism="Arabidopsis thaliana"
/db_xref="taxon:3702"
/chromosome="V"
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Pred. No. 8.5e-32;
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/gene="MFB13.22"
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Best Local Similarity 61.4%;
Matches 296; Conservative
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AY062638
Arabidopsis thaliana Unknown protein (MRI12.1) mRNA, complete cds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (dases 1 to 1307)
Southwick, A., Karlin-Neumann, G., Nguyen, M., Lam, B., Miranda, M., Palm, C.J., Bowser, L., Jones, T., Banh, J., Carninci, P., Chen, H., Cheuk, R., Chung, M.K., Hayashizahi, Y., Ishida, J., Kamiya, A., Kawai, J., Kim, C., Lin, J., Liu, S. X., Narusaka, M., Pham, P.K., Sakano, H., Sakurai, T., Satou, M., Seki, M., Shinn, P., Yamada, K., Shinozaki, K., Ecker, J., Theologis, A. and Davis, R.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Stanford University, 855 California Avenue, Palo Alto, CA 94304
                                                                                                                                                    130 ggtggaggcaaagttgcctccgggattcagatttcacccgaaggacgatgagettgtctg 189
                                                                                                                                                                                                                                                                                 313 AACTCACTACCTCAAAGAGAAGGTCTTCAACATCCGATTTACCGCGGCAGCGATTGGTCA 372
                                                                                                                                                                                                                                                                                                                            ggattggtatttctacagccaaagagaccgaaaatacgcgacggggctgagaactaaccg 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         486
                                                                                                                                                                                         256 GGAGGTGGTGGATTTGCCTCCGGGGTTTCGGTTTCACCCTACTGATGAAGAGATAAT--- 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGAGTTTTACTTTTTCTGCCAGAGGGATCGGAAGTATCCGACCGGGATGAGGACGAACCG 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        370 agcaacggccaccggatattggaaagccaccggcaaagaca---gaaccattctaagaaa 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGCGACCGTGTCTGGTATTGGAAGGCGACGGGAAGGACAAGGAGACTCTTTAGAGGCAA 552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       613 TGAAAAGACCAATTGGGTTATGCATGAATATCGTCTTGATGGA---AAATATTCTTATCA 669
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                                                                                                                                                                                                                                       190 cgattacttgatgagacgatcgcttcacaataatcatcgaccacctcttgtcctgatcca
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                                                                     Length 1471;
                                                                                                            0; Mismatches 170; Indels
                                                                   Score 157; DB 8;
Pred. No. 1.8e-30;
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                                                                12.2%;
62.5%;
                                                                                                          Matches 298; Conservative
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                                                                                       Best Local
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The Salk, Stanford, PGEC (SSP) Consortium members carried out the

sequencing and annotation of the RAFL cDNAs: Nguyen, M.,

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GYWKATGKDKEIFKGKSLVGMKKTLVFYKGRAPKGVYTNWVMIETYRLEGKFAIDNLSK
TAKNECVISRYFHTRIDGTKEHMSVGLPPLMDSSPYLKSRGDSLAGTTLGGLLSHVT
FYSDGTTDROKSLVADFKTTMFGSGSTNFLPNIGSLLDFDPLFLQNNSSVLKMLLDNEE
TOFKKRLHNGGSSESTLASSWQGHNSYGSTGPVNLDCVWKF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="MDYKVSRSGEIVEGEVEDSEKIDLPPGFRFHPTDEELITHYLRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KVVNSFFSAIAIGEVDLNKVEPWDLPWKAKLGEKEWYFFCVRDRKYPTGLRTNRATKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3;
  Southwick, A., Karlin-Neumann, G., Lam, B., Miranda, M., Palm, C.J., Bowser, L., Jones, T., Bann, J., Chen, H., Cheuk, R., Chung, M.K., Kim, C., Lin, J., Liu, S.X., Pham, P.K., Sakano, H., Shinn, P., Yamada, K., Ecker, J., Theologis, A. and Davis, R.W.
                                                                                                                       contributed
                                                                                                           Southwick, A., (SSP/Stanford) and Seal, F. (Mine. Coll.) equally to this work. Shinozaki, K. (RIKEN GSC) and Davis, R.W. (SSP/Stanford) contributed equally to this work as PIS. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               293 ATTGGTGAAGTTGATCTCAACAAGTCGAGCCTTGGGACTTGCCTTGGAAGGCTAAGCTT 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62 aaacctagaaaaaaaaggatcaaatcatggagacggaagaagagagatgaaggaaagtagt 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 118 AATCGCTGAAATGGATTACAAGGTATCAAGAAGTGGGGAGATAGTAGAAGGAGAAGTAGA 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              122 ataagcatggtggaggcaaagttgcctccgggattcaqattcacccgaaggacgatgag 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             178 AGATICA --GAAAAGATIGATITACCACCIGGITICAGAITICACCCAACIGAIGAAGAA 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             182 cttgtctgcgattacttgatgagacgatcgcttcacaataatcatcgaccacctcttgtc 241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         242 ctgatccaagtcgatctcaacaagtgtgagccttgggacatcccaaaaatggcatgcgtg
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                                                                                                                                                                                                                                                                                                                       /note="This clone is in pBluescript
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                                                                                                                                                                                                                                  /organism="Arabidopsis thaliana"/db_xref="taxon:3702"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="Unknown protein"
Karlin-Neumann, G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /protein_id="AAL32716.1"
/db_xref="GI:17065124"
                                                                                                                                                                                                                                                                               /chromosome="III"
/clone="RAFL11-06-110"
                                                                                                                                                                                                                                                                                                                                                       ecotype: Columbia"
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Southwick, A.,
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Alabydlnkcepwelpekakmcekemyffslkdprkyptglrtnrateagywkatgkdr
Elyssktsalvgmkktlufyrgrapfgeksnwvmheyrldgrfayhylsrsskdewvl
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ASKKBHVSCFSTISPPSFDPSSVFDISSNSNTLHSLPAPSFSAILDPSSTFSRNSVFP
SLRSLQENLHLPLFSGGTSAMHGGFSSPLANWPVPETQKVDHSELDCMMSY"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (15-OCT-1999) B.J. Souer, Free University, Dept.Genetics, De Boelelaan 1087, 1081 HV Amsterdam, NETHERLANDS On Oct 19, 1999 this sequence version replaced gi:1321923.

Location/Qualifiers
                                                                                                                                                 PLN 15-0CT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E.J. Souer, Free University, Dept.Genetics,
                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                          Spermatophyta; Magnollophyta; eddicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Petunia.

[ bases 1 to 1173]

Souer, E., van Houwellngen, A., Kloos, D., Mol, J. and Koes, R.

The no apical meristem gene of Petunia is required for pattern primordia boundaries

primordia boundaries

[ cell 85 (2), 159-170 (1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31 GATTCAAATCTTCCCCCTGGCTTTAGGTTCCATCCAACTGAAGAGGCTCATCACTTAC
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/function="apical meristem formation"
                                                                                                                                                       INRNA
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                                                                                                                                                   PHRNANAM 1173 bp ml
P.hybrida mRNA encoding NAM protein.
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/db_xref="G1:6066595"
/db_xref="SPTREMBL:Q40894"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:4102"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (11-OCT-1995)
De Boelelaan 1087, 1081
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Petunia x hybrida
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1 (bases 1 to 1100)
Whitelaw, C.A., Lyssenko, N.N., Thai, V.K., Nath, P. and Tucker, M.L. Functional analysis of regulatory elements in the gene promoter for an abscission-specific cellulase from bean (Phaseolus vulgaris) and characterization of candidate transcription factors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Phaseolus vulgaris
bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
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Whitelaw,C.A. and Tucker,M.L.
Direct Submission
Submitted (25-JUL-2001) Soybean Genomics and Improvement Lab, USDA/ARS, BARC-west, 10300 Baltimore Avenue, Beltsville, MD 20705,
                                                                                                                                                                                                                                                                                                      428 ggtaagctagttgggatgaggaagacattggttttctatcaaggtcgagctcctcgaggc 487
254 gatotoaacaagtgtgagoottgggacatoocaaaaatggcatggtgggagggaaggat 313
                                                                                               tggtatttetacagecaaagagacegaaaataegegaeggggetgagaaetaaeegagea 373
                                                                                                                                 374 acggccaccggatattggaaagccaccggcaaagacagaaccatt----ctaagaaag 427
                                                                                                                                                                                                                              328 AGIGCACITGIIGGGAIGAAGAAACCCIAGIIITCIAICGIGGAAGAGCICCAAAAGGA 387
                                                                                                                                                                                                                                                                                                                                                                                                     488 cgtaaaaccgattgggtcatgcacgaattccgtctccaaggatctcatcatcctccaat 547
                                                                                                                                                                                                                                                                                                                                                                                                                                                       388 GAAAAAAGCAACTGGGTTATGCATGAATATCGCCTTGACGG---CAAATTTGCTTACCAC 444
                                               148 GACCTCAACAAATGCGAGCCATGGGAACTCCCTGAGAAAGCAAAGATGGGAGAAAAAAGAG 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Phaseolus vulgaris NAC domain protein NAC2 mRNA, complete cds. AF402603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          548 cattetetgagetetecaaaaggaagactgggtettgtgtagggtattecataagaat 604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="leaf abscission zone"
64. .834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Phaseolus vulgaris"
/cultivar="red kidney"
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ACCESSION
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* NOTE: This is a 'working draft' sequence.
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NOTE: It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza
                                                                                                          89 TCCCCCCTGGCTTTAGGTTTCACCCAACGGACGAACTAATCGTCTACCTTTGCA 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                              204 gacgatcgcttcacaataatcatcgaccacctcttgtcctgatccaagtcgatctcaaca 263
                                                                                                                                                                                                                                                               agigidagocitigggacatcccaaaaatggcatgcgtgggagggaaggattggtatttct 323
                                                                                                                                                                                                                                                                                        324 acagccaaagagaccgaaaatacgcgacggggctgagaactaaccgagcaacggccaccg 383
                                                                                                                                                                                                                                                                                                                                                                                          266 TTAGTCCACGAGAGAGGAGGTACCCAAACGGGGTGAGGCCTAACCGAGCAACAGTATCTG 325
                                                                                                                                                                                                                                                                                                                                                                                                                                       gatattggaaagccaccggcaaagacagaaccattctaagaaagggtaagctagttggga 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           444 tgaggaagacattggttttctatcaaggtcgagctcctcgaggccgtaaaaccgattggg 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 386 TGAAGAAATCCCTAGTATTTTACAAGGGTAGGCCACCAAAAGGTGACAAGACTGATTGGA 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               504 tcatgcacgaattccgtctccaaggatctcatcatcc---tcccaatcattctctgagct 560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       446 TTATGCATGAGTACCGATTGGCAGAATCAAAACAACCAGTTAACAGGAAAATTGGGTCCA 505
                                                                                        144 tgcctccgggattcagatttcacccgaaggacgatgagcttgtctgcgattacttgatga 203
                                                                                                                                                                                                                  149 ACCAAGC --- CACATCAAAGCCTTGCCCTGCTTCCATCATCCCAGAAGTGGATCTCTACA 205
                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AP003542 147640 bp DNA linear HTG 26-P
Oryza sativa chromosome 6 clone P0589C03, *** SEQUENCING IN
PROGRESS ***, in ordered pieces.
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Oryza sativa nipponbare(GA3) genomic DNA, chromosome 6,
Length 1100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oryza satīva (cultivar:Nipponbare) DNA, clone:P0589C03.
Oryza satīva
                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   561 ctccaaaggaagactgggtcttgtgtagggtattccataagaata 605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           506 TGAGGCTGGATGACTGGGTCTTGTGAGAATTTATAAGAAGAAGA 550
  DB 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Published Only in DataBase (2001) In press 2 (bases 1 to 147640)
  Score 143.4; DB 8;
Pred. No. 6.8e-27;
0; Mismatches 181;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sasaki, T., Matsumoto, T. and Yamamoto, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AP003542.1 GI:13810548
  11.1%;
59.8%;
                                        Matches 278; Conservative
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                        Best Local Similarity
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  Query Match
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AP003542/c
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by the finished sequence as soon as it is available and the accession number will be preserved.

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L SUBMITTER (30-JAN-2002) Takuji Sasaki, National Institute of Agrobiological Sciences, Rice Genome Research Program; Kannondai 2-1-2, Takuba, Ibaraki 305-8602, Japan (E-mall:tsasakienias.affrc.go.ip, URL:http://rgp.dna.affrc.go.ip/, Tel:#1-298-38-7441, Fax:#1-298-38-7468)

NOTE: It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is a vailable and the accession number will be preserved.

* NOTE: This is a "working draft' sequence.
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Sasaki, T., Matsumoto, T. and Yamamoto, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oryza sativa chromosome 6 clone OSJNBa0021N09, *** SEQUENCING IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   55405 GGAGTACTACTACAGCCTCCGCGACCGCAAGTACCCCACGGGACTCCGCACCAACCG 55346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             55285 CACCGGCGCCCTCGTCGGCATGAAGAGCCCTCGTCTTCTACCGCGGCCGCGCCCCCAA 55226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   55466
                                                                                                                                                                                                                                                                                                                                                                                                                                           130 ggtggaggcaaagttgcctccgggattcagatttcacccgaaggacgatgagcttgtctg 189
                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Oryza sativa (cultivar:Nipponbare) DNA, clone:OSJNBa0021N09.
Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         190 cgattacttgatgagacgatcgcttcacaataatcatcgaccacctcttgtcctgatcca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          55465 GATCGACCTGAACAAGTGCGAGCCGTGGGAGCTGCCGGAGAAGGCCAAGATGGGGGGAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            55345 CGCCACGGCCGCCGGCTACTGGAAGGCCACCGGCAAGGACCGCGCGAGATCCGCAGCGCCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                55522 CTACTACCTGCTGCGGAAGGTGGTGGACGGGAGCTTCAACG----GGCGCGCCATCGCGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 310 ggattggtatttctacagccaaagagaccgaaaatacgcgacggggctgagaactaaccg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      424 aaagggtaagctagttgggatgaggaagacattggttttctatcaaggtcgagctcctcg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  370 agcaacggccaccggatattggaaagccaccggcaaagacagaaccattctaa----g
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                                                                                                                                                                                                                                                                                                                       Length 147640;
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                                                                                                                                                                                                            others
                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches 140; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   55225 GGCCAGAAGACCCAGTGGGTCATGCACGAGTACCGCCTCGACG 55181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    484 aggccgtaaaaccgattgggtcatgcacgaattccgtctccaagg 528
                                                                                                                                                                                                            250
                                                                                                                                                                                                                                                                                                                       Score 143; DB 2;
Pred. No. 7.2e-27;
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                                                          /organism="Oryza sativa"
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                                                                                  /cultivar="Nipponbare"/db_xref="taxon:4530"
Location/Qualifiers
1. .147640
                                                                                                                                                                           /clone="P0589C03"
                                                                                                                                               /chromosome="6"
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                                                                                                                                                                                                                                                                                                                       11.1%;
63.2%;
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TITLE
JOURNAL
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Yamada,K., Liu,S.X., Pham,P.K., Banh,J., Banno,F., Dale,J.M.,
Goldsmith,A.D., Jiang,P.X., Lee,J.M., Onodera,C.S., Quach,H.L.,
Tang,C., Toriumi,M., Yamanura,Y., Yi,G., Yu,S., Bowser,L.,
Carninci,P., Chen,H., Cheuk,R., Hayashizaki,Y., Ishida,J.,
Jones,T., Kamiya,A., Karlin-Neumann,G., Kawai,J., Kim,C.,
Koesema,E., Lam,B., Lin,J., Meyers,M.C., Miranda,M., Narusaka,M.,
Nguyen,M., Palm,C.J., Sakurai,T., Sakuu,M., Seki,M., Shinn,P.,
Southwick,A., Tracy,S.E., Shinozaki,K., Davis,R.W., Ecker,J.R. and
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Eukaryota; Viridiplantae; Streptoph/ta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosida II; Brassicales; Brasslcaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AY051015 838 bp mRNA linear PLN 26-AUG-2
Arabidopsis thaliana unknown protein (F10D13_14) mRNA, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                             249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             370 agcaacggccaccggatattggaaagccaccggcaaagacagaaccattctaa----g 423
                                                                                                                                                                                                                                                                                                                                                               ggtggaggcaaagttgcctccgggguttcagatttcacccgaaggacgatgagcttgtctg 189
                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Full Length cDNA of gene F10D13_14 (GI:12597796)
Unpublished
2 (bases 1 to 838)
Yamada,K., Liu,S.X., Pham,P.K., Banh,J., Banno,F., Dale,J.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         190 cgattacttgatgagacgatcgcttcacaataatcatcgaccacctcttgtcctgatcca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    54260 CTACTACCTGCTGCGGAAGGTGGTGGACGGGAGCTTCAACG---GGCGCGCGCATCGCGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ggattggtatttctacagccaaagagaccgaaaatacycgacggggctgagaactaaccg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    54437 CGCCACGGCGCCGCTACTGGAAGGCCACCGGCAAGGACCGCGAGATCCGCAGCGCCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             424 aaagggtaagctagttgggatgaggaagacattggttrtctatcaaggtcgagctcctcg
by the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                     6
                                                                                                                                                                                                                                                                       Length 157274;
                                                                                                                                                                                         104 others
                                                                                                                                                                                                                                                                                                                   0; Mismatches 140; Indels
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                                                                                                                                                                   /clone="OSJNBa0021N09"
32549 c 33321 g 45359 t
                                                                                  /organism="Oryza sativa"
                                                                                                  /cultivar="Nipponbare"
/db_xref="taxon:4530"
/chromosome="6"
                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AY051015
AY051015.1 GI:15293162
                                                                                                                                                                                                                                                                                                                     Matches 256; Conservative
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AY051015
LOCUS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AUTHORS
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                                           FEATURES
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/translation="MEVTSQSTLPPGFRFHPTDEELIVYYLRNQTMSKPCPVSIIPBV
DIYRDPWQDDEFTPEGENEWYFFSPRRYFPWGVRPRNAAVSGSVWAATGTDRAJHSG
SSNVGVKRALVPYKGRPKGIKTDWINHEYRLHDSRRASTRNGSMRLDEWVLRIYK
KRASKLLNEGEGFMDEVLMEDETKVVVNEAERRTEEEIMMWTSMKLP
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Goldsmith, A.D., Jiang, P.X., Lee, J.M., Onodera, C.S., Quach, H.L., Tang, C.C., Toriumi, M., Yamamura, Y., Yu, G., Yu, S., Bowser, L., Carninci, P., Chen, H., Chenk, R., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Kim, C., Koseema, E., Lam, B., Lin, J., Meyers, M.C., Miranda, M., Narusaka, M., Nguyen, M., Palm, C.J., Sakurai, T., Satou, M., Seki, M., Shinn, P., Southwick, A., Tracy, S.E., Shinozaki, K., Davis, R.W., Ecker, J.R. and
                                                                                                                                                                                                                              Theologis, A.

Direct Submission
Submitsed (01-A0G-2001) Plant Gene Expression Center, 800 Buchanan
Street, Albany, CA 94710, USA
The RIKEN Genomic Sciences Center (GSC) members carried out the
collection and clustering of RAFL cDNAs (RAFL cDNA : RIKEN
Arabidopsis Full-Length cDNA'): Seki, M., Narusaka, M., Ishida, J.,
Satou, M., Kamiya, A., Sakurai, T., Carninci, P., Rawai, J.,
Hayashizaki, Y. and Shinozaki, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The Salk, Stanford, PGEC (SSP) Consortium members constructed and sequenced the pUNI (ORF) clones using the RAFL CDUAS: Yamada.K., Liu,S.X., Pham,P.K., Banh,J., Banno,F., Dale,J.M., Goldsmith,A.D., Jiang,P.X., Lee,J.M., Onodera,C.S., Quach,H.L., Tang,C.C., Toriumi,M., Yamamura,Y., Yu,G., Yu,S., Bowser,L., Chen,H., Lorek,R., Jones,T., Karlin-Neumann,G., Kim,C., Koesema,B., Lin,J., Meyers,M.C., Millan-Neumann,G., Yalm,C., Schom,P., Southwick,A., Tracy,S.E., Davis,R.W., Ecker,J.R. and Theologis,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yamada,K. (SSP/PGEC) and Seki, M. (RIKEN GSC) contributed equally to this work. Shinozaki,K. (RIKEN GSC) and Theologis,A. (SSP /PGEC) contributed equally to this work as PIs. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             144 tgcctccgggattcagatttcacccgaaggacgatgagcttgtctgcgattacttgatga 203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26 TCCCTCCAGGGTTCAGATTTCATCCTACCGACGAGGAAC---TCATCGTTTACTATCTTC 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MDYMGPVSHIDNFSQFDHLHQPDSESSWFGDLQFNQDEILNHHRQAMFKF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          204 gacgatcgcttcacaataatcatcgaccacctcttgtcctgatccaagtcgatctcaaca
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Arabidopsis thaliana"
/db_xref="taxon:3702"
/chromosome="1"
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ecotype: Columbia"
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/product="unknown protein"
/protein_id="AAK93692.1"
/db_xref="GI:15293163"
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168 c 191 g
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us-09-889-926-1.rge

/Lote="This close is in amodified pBluescript vector (FLC-1) as a BamHI/XhoI insert.

/organism="Arabidopsis thaliana" /db\_xref="taxon:3702"

source

/chromosome="1" /clone="RAFL09-16-111 (R09158)"

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Yamda,K., Liu,S.X., Sakano,H., Pham,P.K., Banh,J., Chung,M.K., Goldsmith,A.D., Lee,J.M., Quach,H.L., Toriumi,M., Yu,G., Bowser,L., Carninci,P., Chen,H., Cheuk,R., Hayashizaki,Y., Ishida,J., Jones,T., Kamiya,A., Karlin-Neumann,G., Kawai,J., Kim,C., Lam,B., Lin,J., Miranda,M., Narusaka,M., Nguyen,M., Palm,C.J., Sakurai,T., Satou,M., Seki,M., Shinn,P., Southwick,A., Shinozaki,K., Davis,R.W., Ecker,J.R. and Theologis,A., Shinozaki,K., Greethaltend
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(bases 1 to 1109)
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RIKEN Genomic Sciences Center (GSC) members carried out the
collection and clustering of RAFL cDNAs (RAFL CDNA : 'RIKEN
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Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J.,
Hayashizaki,Y. and Shinozaki,K.
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Arabidopsis thaliana unknown protein (F10D13_14) mRNA, complete
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                                                                                                  203 TCAGCCCTAGAGAAAGAAATATCCAAACGGAGTCAGACCAAACCGGGCAGCTGTTTCCG 262
                                                                                                                                                                                                          gatattggaaagccaccggcaaagacagaaccattctaagaaagggtaagctagttggga 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           383 TCATGCATGAGTATCGTCTCCATGATTCACGTAAAGCATCAACGAAACGTAACGGTTCCA 442
324 acagecaaagagacegaaaataegegaeggggetgagaaactaaeegageaaeggeeaeeg 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               564 caaag---gaagactgggtcttgtgtagggtattccataaga 602
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Pred. No. 1.6e-26;
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Yamada,K. (SSP/PGEC) and Seki,M. (RIKEN GSC) contributed equally to this work. Shinozaki,K. (RIKEN GSC) and Theologis,A. (SSP/PGEC) contributed equally to this work as PIs. Location/Qualifiers

The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAFL CDNAS: Yamada,K., Liu,S.X., Sakano,H., Pham,P.K., Banh,J., Chung,M.K., Goldsmith,A.D., Lee,J.M., Quach,H.L., Toriumi,M., Yu,G., Bowser,L., Chen,H., Cheuk,R., Jones,T., Karlin Neumann,G., Kim,C., Lam,B., Lin,J., Miranda,M., Nguyen,M., Paln,C.J., Shin,P., Southwick,A., Pavis,R.W., Ecker,J.R. and Theologis,A.

FEATURES

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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- nucleic search, using sw model OM nucleic

July 15, 2002, 06:40:44; Search time 1596.85 Seconds (without alignments) 10878.029 Million cell updates/sec Run on:

US-09-889-926-1 1287 Title:

1 gtcgaccacgcctccgtctt.....aaaaaaaaaagggcggccgc 1287 Perfect score: Sequence:

IDENTITY\_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

13736207 segs, 6748477542 residues Searched:

27472414 Fotal number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Listing first 45 summaries Post-processing: Minimum Match 0% Maximum Match 100%

Database :

EST:\*

1: em\_estba:\*
2: em\_esthum:\*
3: em\_estin:\*
4: em\_estin:\* em\_estov:\* em\_estpl:\* em\_estro:\* em\_htc:\* gb\_est1:\* gb\_est2:\* 10: 11: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

em\_gss\_inv:\* em\_gss\_pln:\* em\_gss\_vrt:\*

em\_gss\_hum:\*

gb\_htc:\* \*:ssb\_dp SUMMARIES

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di ib	12 B08241		12 B08263	AV536694	AV538912	.2 B10411	12 B11695	.0 BM112823	.0 BI123181	.0 BE555459	.0 BM112826	10 BI122890	.0 BG791220	AW234514	.0 BE554923	.0 BI123635	AW685143
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201.6	198.8	197.6	183.2	169.4	168.4	166.8	165.8	165.8	165.2	161.8	158.2	157	155.4	155.2	148.6	148.2	147	143.6	142.8	4	142	140.8	140.4	140.4	140.4	140	139.4
18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

B08241 1132 bp DNA linear GSS 14-MAY-1997 F23117-Sp6.1 IGF Arabidopsis thaliana genomic clone F23117, DNA Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosida; II; Brassicales; Brassicaceae; Arabidopsis.

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BAC End Sequences at ATGC
Unpublished (1997)
Other GSSs: F2317-T7.1, F23117-T7, F23117-Sp6
Contact: Ecker J.
Arabidopsis Thaliana Genome Center
University of Pennsylvania
Dept. of Biology, University of Pennsylvania, Philadelphia, PA
19104 Email: jecker@atgenome.bio.upenn.edu
Seq primer: Sp6
Class: BAC ends
High quality sequence start: 93
High quality sequence stop: 846.
Location/Qualifiers

i. 1132

/organism\_"Arabidopsis thaliana" /strain="Columbia" /db\_xref="taxon:3702" B08241 B08241.1 GI:2089363 thale cress. Arabidopsis thaliana Tel: 215-898-9384 Fax: 215-898-8780 sequence. source SOURCE DEFINITION TITLE JOURNAL COMMENT ACCESSION REFERENCE AUTHORS VERSION KEYWORDS FEATURES RESULT B08241

us-09-889-926-1.rst

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Page

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A large scale analysis of cDNA in Arabidopsis thaliana: Generation of 12,028 non-redundant expressed sequence tags from normalized and size-selected_CDNA_libraries
                                                                                 The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 153-3, Kisazusa, Chiba 292-0812, Japan
Email: asamizu@Kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
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Contact: Erika Asamizu
                                                                                                                                                                                                                                                                                           132 C
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                                                                                                                                                                                                         cttacatcaactttgaccaagaaccctcttcttatctcagtgatgatcatcactacatca 746
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                                                                        Score 615.8; DB 12;
Pred. No. 8.1e-100;
       Produced by Thomas Altmann"
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B08263 114-MAY-1997 IGF Arabidopsis thaliana genomic clone F27J24, DNA
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Eukaryota; Viridiplantae: Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae: eurosidas II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 1142)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /sex="hermaphrodite"
/note="Vector: BeloBACII; Site_1: ECORI; Site_2: ECORI;
Produced by Thomas Altmann"
a 282 c 217 g 331 t 2 others
                                                                                                                                                                                                                    Feng, J., Dewar, K., Buehler, E., Kim, C., Li, Y., Shinn, P., Sun, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dept. of Biology, University of Pennsylvania, Philadelphia, PA
19104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Arabidopsis thaliana"
                                                                                                                                                                                                                                                                                                                                                                                                            Email: jecker@atgenome.bio.upenn.edu
Seq primer: Sp6
                                                                                                                                                                                                                                                                                                               Arabidopsis Thaliana Genome Center
                                                                                                                                                                                                                                                                 Unpublished (1997)
Other_GSSs: F27J24-T7, F27J24-Sp6
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High quality sequence stop: 816.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                 University of Pennsylvania
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                                                                                                                                                                                                                                   Ecker, J.
BAC End Sequences at ATGC
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/clone_lib="IGF"
                                                                           B08263
B08263.1 GI:2089385
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Best Local Similarity 90.33
Matches 645; Conservative
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1 (bases I to 482).
Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S.
A large scale analysis of cDNA in Arabidopsis thaliana: Generation of 12,028 non-redundant expressed sequence tags from normalized and size-selected cDNA libraries
DNA Res. 7, 175-180 (2000)
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
                                                                                                                         987 cacagagttatggagaaggtagctcggagagcctcctgaccgacatcggtattccaagca 1046
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               682 CACAGAGTTATGGAGAAAGGTACTCGGATAGCTTCCTGACCGACATCCGTATCCCAACCA 741
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The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
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/organism="Arabidopsis thaliana"
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Pred. No. 1.1e-52;

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Best Local Similarity
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Asamizu.E., Nakamura,Y., Sato,S. and Tabata,S.
A large scale analysis of CDNA in Arabidopsis thaliana: Generation of 12,028 non-redundant expressed sequence tags from normalized and size-selected cDNA libraries
DNA Res. 7, 175-180 (2000)
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Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL:htrp://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
                                                                                                                                                                                                                                                                                       ttcacaataatcatcgaccacctcttgtcctgatccaagtcgatctcaacaagtgtgagc 272
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/clone="RZ124b03F"
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[ pases 1 to 1026]
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                                                                                                                                                                                                                                                                                           958 gattgatggaagcctcgggcctaaagaatcacagagttatggagaaggtagctcggagag 1017
                                                                                                                                                                                                               Dept. of Biology, University of Pennsylvania, Philadelphia, PA 19104
                                                              291 GATTGATGGAAGCCTCGGGCCTAAAGAATCACAGAGTTATGGAGAAAGGTAGCTCGGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                  1198 aaataccacttatgacgctagacatacatatttcatcgtagttccattt 1248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        72 others
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Other_GSSs: F23117-T7.1, F23117-Sp6.1, F23117-T7
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/organism="Arabidopsis thaliana"
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272 c 170 g 244 t
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Seq primer: Sp6
100.0%; Pred. ....
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High quality sequence stop: 229.
Location/Qualifiers
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B10411
B10411.1 GI:2091692
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                          Matches 351; Conservative
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Fax: 215-898-8780
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  669 GTCTCAAAGCTCTACTCAGTCAGCTCACTAAAATGATGAAAGCCTCCGGCCT-AAGAAT 727
                                                                   567 aggaagactgggtcttgtgtgtagggtattccataagaatacggaaggagttatatgtagag 626
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                                                                                                                                                                                                                                                                                                          489 TCAATGAGCACGTACCCCTGCTCTCCANTNTGTCACAGAANCANACCTTANACTCGAAAC
                                                                                                                                                                                                        cttacatcaactttgaccaagaaccctcttcttatctcagtgatgatcatcactacatca
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 Score 337.6; DB 12; Length 1026;
                                 Indels

    1069
/organism="Arabidopsis thaliana"

                Pred. No. 1.7e-50;
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Seq primer: Sp6
                                0; Mismatches
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Other_GSSs: F27J24-Sp6.1, F27J24-T7
Contact: Ecker J.
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High quality sequence stop: 490.
Location/Qualifiers
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/db_xref="taxon:3702"
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85.6%;
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Arabidopsis thaliana
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B11695
B11695.1 GI:2092828
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                                Matches 375; Conservative
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1 (bases 1 to 739)
van der Hoeven, R., Sun, H., Karamycheva, S.A., Tsai, J., Van Aken, S.,
                          /sex="hermaphrodite"
/sex="hermaphrodite"
/note="Vector: BeloBACII; Site_1: EcoRI; Site_2: EcoRI;
Produced by Thomas Altmann"
a 235 c 20 g 360 t 99 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1047 ctgtttggaattgctgatgatcgagtgtaacgagagttactattgctatattcctatcca 1106
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                                                                                                                                                                           0; Mismatches 182;
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Pred. No. 5.9e-46;
               /clone_lib="IGF"
/clone="F27J24"
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                                                                                                                                           Match 24.28;
Local Similarity 69.78;
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Unpublished (2001)
Contact: Erlandsson R
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Best Local Similarity 73.3%;
Matches 311; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     caataatcatcgaccacctcttgtcctgatccaagtcgatctcaacaagtgtgagccttg 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             316 CACCGGAAAAGATCGTGCAATAATCAGAAAAGGAAGTCTTGTAGGAATGAGGAAAACCCT 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ccgtctccaaggatctcatcatcctcccaatcattctc---tgagctctccaaaggaaga 573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   436 CCGCCTTGATGAAGGTCCCCTTAGTAACATTCGTTCTCAAAATTTCTTCTCTCAAGGAGGA 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          619 atgtagagacaacatgggaagctgttttgatgagacagcctctgcatcgcttcctccact 678
Chiemingo, A., Bougri, C., Buell, C.R., Ronning, C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100 agaagagatgaaggaaagtagtataagcatggtggaggcaaagttgcctccgggattcag 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   136 CACAGACCAACAATACCCTCTTCTCATAGAAGTTGACCTCAATAAATCCGAACCTTG 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ccgaaaatacgcgacgggctgagaactaaccgagcaacggccaccggatattggaaagc 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          256 CCGAAAATACGCGACGGGGTCCGAACAAACAGGCCACCGTATCTGGTTACTGGAAAGC 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             caccggcaaagacagaaccattctaagaaagggtaagctagttggggatgaggaagacatt 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                376 AGTITICIATCAAGGAAGAGCCCCAAAAGGAAGAAAAGTGATTGGGTTATGCATGAATT 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16 AAAAATGAGTAACAACAGCTGAGCATGGTGGAATCCAAATTACCACCAGGATTTAG 75
                                                               Contact: Research Genetics, Libraries Division
Tel: 1-800-711-6195
Email: cdna@resepn.com
For clone info: please contact Research Genetics, Libraries
Division tel 1-800-711-6195, email cdna@resgen.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ggttttctatcaaggtcgagctcctcgaggccgtaaaaccgattgggtcatgcacgaatt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           574 ctgggtcttgtgtagggtattccataagaatacggaaggagtt-----at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 10; Length 739;
                                                                                                                                                                                                                                                                                               /tissue_type="roots"
/dev_stage="in vitro grown stem cuttings"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches 229; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 2.3e-35;
                                                                                                                                                                                                      /organism="Solanum tuberosum"
/cultivar="Rennebec"
/db_xref="taxon:4113"
              Tanksley, S. and Baker, B. Generation of ESTs from potato roots
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 252.6;
                                                                                                                                                                                                                                                                             /clone_lib="potato roots"
                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                             /clone="cPR016A9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19.68;
64.78;
                                                    Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 465; Conservative
                                                                                                                                                       Seq primer: T3.
Utterback, T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                     251
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EST 31-DEC-2001
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Hertzberg,M., Aspeborg,H., Erlandsson,R., Bjorkbacka,H., Hiltonen
T., Karlsson,J., Teerl,T., Gustafsson,P., Bahlerao,R., Jansson,S.,
Nilsson,O., Sundberg,B., Nilsson,P., Uhlen,M., Sandberg,G. and
Lundeberg,J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Populus tremula x Populus tremuloides.

Populus tremula x Populus tremuloides
Eukaryota; Viridiplantaea Streptopophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Malpighiales; Salicaceae; Populus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    171
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                                                                                                                          ctacatcatcaatgagcacgtacctgcttctccaatttgtcacagaaccaaaccttaa 797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             105 agatgaaggaaagtagtataagcatggtggaggcaaagttgcctccgggattcagatttc 164
                                                                                                                                                                                    672 IGAATTATATTATGAGCCAGTGCCCTGCTTTCTCATTTTCACCCTAACCAAACTTTCA 730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                               BI123181 494 bp mRNA linear EST 31-DE 1018P65P Populus leaf cDNA library Populus tremula x Populus
gatggatcettacatcaactttgaccaagaaccetettetteteteagtgatgatcatea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               225 atcgaccacctcttgtcctgatccaagtcgatctcaacaagtgtgagccttgggacatcc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               172 ACTGCGACTCCCTTCTCATGATAGAGGTCGACCTCAACAAGTGTGAGCCTTGGGATATTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      285 caaaaatggcatgcgtgggagggaaggattggtatttctacagccaaagagccgaaaat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     405 aagacagaaccattctaagaaagggtaagctagttgggatgaggaagacattggtttct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Populus tremula x Populus tremuloides" /db_xxref="taxon:47664" /clone_lib="Populus leaf cDNA library" /note="Organ: leaf"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 ATCCAAGAGATGAAGAGCTTGTATGTGATTACTTGATGA-----AGAAGGCTTCTC
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Pred. No. 3.1e-31;
0; Mismatches 104; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Royal Institute of Technology
Teknikringen 30, Stockholm S-10044, Sweden
TPE1: 46 8 790 8287
Fax: 46 8 245452
                                                                                                                                                                                                                                                                                                                                                                                                         tremuloides cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: rikerl@biochem.kth.se.
Location/Qualifiers
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BI123181.1 GI:18007156
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9; Gaps

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416 attctaagaaagggtaagctagttgggatgaagaagacattggtttctatcaaggtcga 475
                                                                                                                                                                                                                                               296 tgcgtggggagggaaggattggtatttctacagccaaagagaccgaaaatacgcgacgggg 355
                                                                                                                                                                                                                                                                                                                                                                                                                                   356 ctgagaactaaccgagcaacggccaccggatattggaaagccaccggcaaagacagaacc 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     111 AGCAACATAAGCATGGTAGAGGCAAAGCTGCCACCAGGATTCAGGTTTCATCCAAGAGAT 170
                                                                                                                                                           176 gatgagettgtetgegattaettgatgagaegategetteacaataateategaecaeet 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                342 TTACGCACAAAATCGTGCCACTGCCTCAGGGTATTGGAAGGCCACAGGGAAGGACAGGCCT 401
                                                                116 agtagtataagcatggtggaggcaaagttgcctccgggattcagatttcacccgaaggac 175
                                                                                                                                                                                                         171 GAAGAGCTTGTGTGTGATTACTTGATGAAGAAGGTGCAACACACAATGAT-----TCC
                                                                                                                                                                                                                                                                                                                                                                     402 ATCCTCCGCAAGGGCACCCATGTAGGGATGGAGAAGACNTTGGTGTTCTATCAAGGAAGG
Pred. No. 1.7e-30;
0; Mismatches 117; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Research Genetics, Libraries Division
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Solanum tuberosum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Generation of ESTs from potato roots
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="potato roots"
/tissue_type="roots"
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/db_xref="taxon:4113"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BM112826.1 GI:17075874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: cdna@resgen.com
71.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     536 catecteceaateattet 553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                522 GGACCTCCTAAAATTTCT 539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: 1-800-711-6195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          end, mRNA sequence.
BM112826
  Best Local Similarity 71.2 Matches 312; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Solanum tuberosum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seq primer: T3.
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Xho1; This cDNA library was constructed from mRNA isolated
from etiolated hypocotyl tissue of 9-10 day old seedlings
of the cultivar Williams 82. Complementary DNA was
synthesized from mRNA using a primer consisting of a
poly(df) primer Williams 81. Complementary DNA fragments
adapters were ligated to the blunt-ended cDNA fragments
followed by digestion with ECORI and XhoI. The CDNA
fragments were directionally cloned into the ECORI.XhoI
restriction site of the pBluescript vector. The ligated
cDNA fragments were transformed into DH10B host cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: est@watson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-533-4363 or contact via email: ccu@resgen.com
Insert Length: 1555 Std Error: 0.00
                                                                                                                                                                                                                                                                                                    BE555459 64-DEC-2001 sp89f05.yl Gm-c1045 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1045-826 5' similar to TR:Q40880 Q40880 NAM GENE. [1] ;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tobses 1 to 640)
Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Thelsing, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohh, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
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                                                                       352 AGGACAGACATATCCTACGTAAGGGAACCCTTGTTGGCATGAGAAAGACCTTGGTGTGT 411
                                               465 atcaaggtcgagctcctcgaggccgtaaaaccgattgggtcatgcacgaattccgtctcc 524
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Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:3847" /clone="GRWOME SYSTEMS CLONE ID: Gm-c1045-826" /clone_lib="Gm-c1045"
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Public Soybean EST Project
Washington University School of Medicine
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BM112826 Totato roots Solanum tuberosum cDNA clone CPR016A15 5'
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1 (bases 1 to 715)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              van der Hoeven, R., Sun, H., Karamycheva, S.A., Tsai, J., Van Aken, S., Utterback, T., Chiemingo, A., Bougri, O., Buell, C.R., Ronning, C., Tanksley, S. and Baker, B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2: XhoI; supplier: Cornell University, Tanksley lab;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 For clone info: please contact Research Genetics, Libraries Division tel 1-800-711-6195, email cdna@resgen.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /dev_stage="in vitro grown stem cuttings"
/lab_host="SOLR"
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DB 10; Length 640;

17.5%; Score 225.2;

Query Match

COMMENT

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sequencing; The Institute for Genomic Research. Roots were
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Hertzberg,M., Aspeborg,H., Erlandsson,R., Bjorkbacka,H., Hiltonen
T., Karlsson,J., Teeri,T., Gustafsson,P., Bahlerao,R., Jansson,S.,
Nilsson,O., Sundberg,B., Nilsson,P., Uhlen,M., Sandberg,G. and
Lundeberg,J.
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Populus tremula x Populus tremuloides
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Malpighiales; Salicaceae; Populus.
                 isolated from in vitro grown stem cuttings on CM medium. Roots were isolated two weeks after placing the stem cuttings from in vitro grown plants on medium."
                                                                                                                                                                                                                                            100 agaagagatgaaggaaagtagtataaagcatggtggaggcaaagttgcctccgggattcag 159
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                                                                                                                                                              Score 217.4; DB 10; Length Pred. No. 4e-29; 0; Mismatches 171; Indels
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BI122890.1 GI:18006865
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Best Local Similarity 67.3%;
Matches 368; Conservative (
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Wang, Y.-H., Garvin, D.F. and Kochian, L.V.
Nitrate-induced genes in tomato roots. array analysis reveals novel genes hat may play a role in nitrogen nutrition
Plant Physiol. 127 (1), 345-359 (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                              69 AGAGAAAGATGAGCAACATAAGCTTCGTGGAGGCAAAACTGCCACCAGGGTTTAGGTTCC 128
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                                                                                                                                                                           /organism="Populus tremula x Populus tremuloides"
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/clone_lib="Populus leaf cDNA library"
/note="Organ: leaf"
Contact: Erlandsson R
Department of Biotechnology
Royal Institute of Technology
Teknikringen 30, Stockholm S-10044, Sweden
Tatl: 46 8 790 8287
Fax: 46 8 245452
                                                                                                                                                                                                                                                                                                                                 DB 10;
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Pred. No. 2.4e-28;
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US Plant Soil & Nutrition Lab
Cornell University
                                                                                                                 Email: rikerl@biochem.kth.se
                                                                                                                                     Location/Qualifiers
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us-09-889-926-1.rst

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This clone is available through: ResGen, Invitrogen Corp. 2130 South Memorial Parkway Huntsville, AL 35801 For further information call: (800)-533-4363 or contact via email: ccu@resgen.com High quality sequence stop; 330.
A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Mailin, J., Bowers Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann Public Soybean EST Project
Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Public Soybean EST Project
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                                                                                                                                                                                                                                                                                                                                         Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA Tel: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="GENOME SYSTEMS CLONE ID: Gm-c1028-16" /clone_lib="Gm-c1028"
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1.6e-27;
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/organism="Glycine max"
/db_xref="taxon:3847"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: est@watson.wustl.edu
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Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          125 AAATGAGTAACAACAGCTTGAGCATGGTGGAATCCAAATTACCACCAGGATTTAGAT 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     162 ttcacccgaaggacgatgagcttgtctgcgattacttgatgagacgatcgcttca---- 216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 212.2; DB 10; Length
Pred. No. 3.5e-28;
0; Mismatches 123; Indels
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    Tower Rd, Ithaca, NY 14853, USA
                                                                                                                                                                                                   Location/Qualifiers
                                     Tel: (607) 255-5445
Fax: (607) 255-1132
Email: lvkl@cornell.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GI:6566882
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70.1%;
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In Dupublished (1999)
Contact: Shoemaker R/Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ## 110 mRNA linear EST 04-DEC-2001 Gm-c104511.71 Gm-c1045 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: BE554923 BE554923.1 GI:9819410
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: est@watson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-533-433 or contact via email: ccu@resgen.com
Insert Length: 1106 Std Error: 0.00
High quality sequence stop: 419.
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
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/lab_host="DH10B"
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215 CTTCTCTTGATAGATGTTGACCTTAACAAGTGTGAGCCATGGGATATTCCTGAAACAGCA
                                                                  tgcgtggggagggattggtatttctacagccaaagagaccgaaaatacgcgacgggg
                                                                                           335 TTACTCACAAATCGTGCCACTGCCTCAAGGTATTGGAAGGCCACATGGAAGGACAGGCCT
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/clone="GENOME SYSTEMS CLONE ID: Gm-c1045-165"
/clone_lib="Gm-c1045"
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(Gibco BRL). This library was constructed by Dr. Randy
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                                                                                                                                                                                    176 gatgagettgtetgegattaettgatgagaegategetteacaataateategaeeaet 235
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                                                                                                                                                                                                                                                        102 GAAGAGCTTGTGTGTGATTACTTGATGAAGGTGCAACACAATGAT-----TCC 152
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2: /SIDSI/gcgdata/hold-geneseq/geneseqn-embl/NA1981.DAT:*
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GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
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P-PSDB; AAB15081. 

Isolated NAC1 gene sequence from Arabidopsis thaliana is used to produce transgenic plants which are larger than the wild type versions

Claim 1; Page 18-20; 35pp; English.

The present sequence is the Arabidopsis thaliana NACl gene. This gene belongs to the NAC family of genes which may play a role in patterning of the shoot and floral meristem. This gene was isolated from an A. thaliana cDNA library expressed in Schizosaccharomyces pombe cells. The present gene may be used for making a genetically altered plant which is larger than a wild type version of the plant by overexpressing NACl. The modified plant produces larger leaves, larger roots and more lateral roots than the wild type version.

Sequence 1287 BP; 386 A; 307 C; 274 G; 320 T; 0 other;

300 360 361 aactaaccgagcaacggccaccggatattggaaagccaccggcaaagacagaaccattct 420 480 480 900 900 099 721 teteagtgatgatcateactacateatcaatgagcacgtaccetgettetecaatttgte 780 tataagcatggtggaggcaaagttgcctccgggattcagattcacccgaaggacgatga 180 241 cctgatccaagtcgatctcaacaaytgtgagccttgggacatcccaaaaatggcatgcgt 300 61 aaaacctagaaaaaaaaaggatcaaatcatggagacggaagaagaggatgaaggaaagtag 120 tataagcatggtggaggcaaagttgcctccgggattcagatttcacccgaaggacgatga 180 Gaps gtogaccacgcctccgtctttatctctcttttcctcttaaccatccactaatcaaacact 60 9 cctgatccaagtcgatctcaacaagtgtgagccttgggacatcccaaaaatggcatgcgt tgcatcgcttcctccactgatggatccttacatcaactttgaccaagaaccctcttctta 1 glogaccacgcctccgtctttatctctctttcctcttaaccatccactaatcaaacact 181 gcttgtctgcgattacttgatgagacgatcgcttcacaataatcatcgaccacctcttgt gggagggaaggattggtatttctacagccaaagagagaccgaaatacgcgacggggctgag 301 gggagggaaggattggtatttctacagccaaagagaccgaaaatacgcgacgggctgag aagaaaagggtaagctagttgggatyaggaagacattggttttctatcaaggtcgagctcc tcgaggccgtaaaaccgattgggtcatgcacgaattccgtctccaaggatctcatcatcc tegaggeegtaaaacegattgggteatgeaegaatteogteteeaaggateteateatee gaatacggaaggagttatatgtagagacaacatgggaagctgttttgatgagacagcctc gaatacggaaggagttatatgtagagacaacatgggaagctgttttgatgagacagcctc ; 0 21; Length 1287; 0; Indels DB 0; Mismatches 100.0%; Score 1287; 100.0%; Pred. No. 0; Best Local Similarity 100. Matches 1287; Conservative Query Match 121 121 481 601 421 481 601 661 241 301 g ò g QQ g Op ò g 염 ò qq ò ò 임 ò ð a ò qq δ ò δ

tgatggaagcctcgggcctaaagaatcacagagttatggagaaggtagctcggagagcct 1020 taccacttatgacgctagacatacatatttcatcgtagttccattgtttcaaaaaaa 1260 teteagtgatgatcateactacateatgageaegtaceetgetteteeaatttgte 780 caagaaccetaaccettgtttactggtggttcagectcagecaegetcacaggectega tgatggaagcctcgggcctaaagaatcacagagttatggagaaggtagctcggagagcct cctgaccgacatcggtattccaagcactgtttggaattgctgatgatcgagtgtaacgag agttactattgctatattcctatccatgattggaacaattcttcggggggaaataacgtg tgcttgtctgattgtacaaacatttcctcactcttgtacccacggtagattcatgtaaaa acagaaccaaaccttaaactcgaacctaaccaactcagtctctgaactcaagattccatg acagaaccaaaccttaaactcgaacctaaccaactcagtctctgaactcaagattccatg caagaaccctaaccccttgtttactggtggttcagcctcagccacgctcacaggcctcga Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss. Arabidopsis thaliana DNA fragment SEQ ID NO: 25930 1261 aaaaaaaaaaaaaaaaaggcggccgc 1287 BP 99US-0126264. 99US-0126785. 99US-0127462. 99US-0128234. 99US-0121825. 99US-0123180. 99US-0123548. 99US-0125788. 99US-0128714. 99US-0129845. 99US-0130077. AAC39794 standard; DNA; 1352 2000EP-0301439 (first entry) Arabidopsis thaliana EP1033405-A2 25-FEB-2000; 23-MAR-1999; 25-MAR-1999; 29-MAR-1999; 17-OCT-2000 05-MAR-1999; 09-MAR-1999; 08-APR-1999 16-APR-1999; 19-APR-1999; 06-SEP-2000 AAC39794; 7 841 1021 1081 1081 1141 1141 721 781 841 901 901 961 961 1021 1201 1201 AAC39794 RESULT g a ŏ QQ QΥ 염 ŏ qq δ ŏ δλ g ò g ŏ ద ŏ ö

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99US-0144352. 99US-0144632. 99US-0144814. 99US-01448114. 99US-0145086. 99US-0145087. 99US-0145087. 99US-0145087. 99US-0145192. 99US-0145192.	990S-0145276. 990S-0145276. 990S-0145913. 990S-0145919. 990S-0145951. 990S-0146388. 990S-0147389. 990S-0147204. 990S-0147302. 990S-0147302. 990S-0147416.	990x-0148341. 990x-0148685. 990x-0149368. 990x-0149426. 990x-0149722. 990x-0149923. 990x-0149923. 990x-0149930. 990x-0150864. 990x-0150864. 990x-0151065. 990x-0151083.	990S-0153070. 990S-0154038. 990S-0154038. 990S-0154039. 990S-0155486. 990S-0155486. 990S-015659. 990S-015629. 990S-0158029. 990S-0158029. 990S-0158029. 990S-0159233.
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caaacatttcctcactcttgtacccacggtagattcatgtaaaataccacttatgacgct 1216
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        ctgatggatccttacatcaactttgaccaagaaccctcttcttatctcagtgatgatcat 744
                                                                                                           925 gatcagatggttctcagagctctactcagtcagctcactaagattgatggaagcctcggg
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                              cactacatcatcaatgagcacgtaccctgcttctccaatttgtcacagaaccaaacctta
                                                 cactacatcatcatgagcacgtaccctgcttctccaatttgtcacagaaccaaacctta
Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
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99US-0123180.
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ive 0; Mismatches
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23-MAR-1999;
25-MAR-1999;
29-MAR-1999;
01-APR-1999;
06-APR-1999;
16-APR-1999;
16-APR-1999;
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                                                                                                                                                           Length 1351;
                                                                                                                                                                       Indels
                                                                                                                                                           DB 21;
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                                                                                                                                                          Score 1203; DB Pred. No. 0; 0; Mismatches
                                                                                   99US-0161404.
99US-0161405.
99US-0161406.
99US-0161359.
99US-0161360.
99US-0161361.
99US-0161923.
                                                                                                                                                          93.5%;
99.3%;
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99US-0160815.
99US-0160980.
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99US-0160767
            99US-0159638
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99US-0160989
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28-0CT-1999;
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990S - 0.1444352 990S - 0.144632 990S - 0.144684 990S - 0.145086 990S - 0.145086 990S - 0.145087 990S - 0.147303 990S - 0.147303 990S - 0.147403 990S - 0.15708 990S - 0.15708	S06
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21 - APR - 1999; 23 - APR - 1999; 23 - APR - 1999; 23 - APR - 1999; 24 - APR - 1999; 26 - APR - 1999; 27 - APR - 1999; 28 - APR - 1999; 29 - APR - APR - 1999; 29 - APR - 1999; 29 - APR - 1999; 29 - APR - 1999;	.JUL-1999 .JUL-1999 .JUL-1999 .JUL-1999 .JUL-1999 .JUL-1999
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                                        atcgagtgtaacgagagttactattgctatattcctatccatgattggaacaattcttcg
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Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
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990S-01318891.
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05 - MAX - 1999;
06 - MAX - 1999;
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11 - MAX - 1999;
14 - MAX - 1999;
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09-MAR-1999;
23-MAR-1999;
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23-APR-1999;
28-APR-1999;
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Pred. No. 4e-256;
0; Mismatches 2; Indels 0;
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99.8%;
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18-007-1999

21-007-1999

21-007-1999

21-007-1999

22-007-1999

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                                                   DB 21; Length 1221;
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                                                   Score 924.4; DB 21 Pred. No. 2.8e-249;
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99US-0161993.
99US-0162142.
                                                   71.8%;
99.6%;
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                                                               Local Similarity
 28-OCT-1999;
28-OCT-1999;
29-OCT-1999;
                                                                             948;
                                                   Query Match
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The present sequence is Arabidopsis thaliana transcription factor cDNA. The transcription factors are used to alter the structure and developmental characteristics of plants such as soybean, wheat, corn, potato, cotton, rice, olised rape, sunflower, alfalfa, sugarcane, turf, banana, blackberry, blueberry, strawberry, raspberry, carrot, cantaloupe, cauliflower, coffee, cucumber, egyphart, grappes, mango, lettuce, honeydaw, melon, onlon, papaya, peas, peppers, pineapple, spinach, squash, sweet corn, tobacco, tomato, watermelon, rosaceous fruits and vegetable brassicas. The transcription factors are specifically useful for modifying traits associated with plant's pathogen tolerance such as alterations in cell wall composition, trichome number or structure, callose induction, phytoalexin conduction, and alterations in the cell death response. Transgenic plants expressing these transcription factors are more tolerant to biotrophic or necrotrophic pathogens such as fundi, bacteria, mollicutes, viruses, nematodes and paramitic higher plants. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acids encoding plant transcription factor polypeptides, useful for altering the pathogen resistance characteristics of plants, e.g. corn, potato and cotton plants
                                                                                                                                                                                                                                                /product= "Arabidopsis thaliana transcription factor"
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                                                                                                           pathogen tolerance; trichome structure; callose induction; phytoalexin induction; plant structure; plant development; ss.
                                                                                               Transcription factor; pesticidal; antimicrobial; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Heard J, Ratcliffe O, Creelman R, Jiang C, Pineda O,
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                                                             Arabidopsis thaliana transcription factor G525 cDNA.
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109..966
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17-APR-2000; 2000US-0197899.
22-AUG-2000; 2000US-0227439.
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                               (first entry)
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RATCLIFFE O.
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PINEDA O.
REUBER L.
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(PINE/) PINEDA O
(REUB/) REUBER L
(ADAM/) ADAM L.
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(RATC/)
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Sequence 1179 BP; 391 A; 223 C; 229 G; 336 T; 0 other;

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                                                                                198 tgatgagacgatcgcttcacaataatcatcgaccacctcttgtcctgatccaagtcgatc 257
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   DB 22; Length 1179;
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                                0; Mismatches 204; Indels
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13.7%; Score 176.6; DB 2
60.7%; Pred. No. 2.6e-39;
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               Best Local Similarity 60.7
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                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                     Score 176.6; DB 21; Length
Pred. No. 2.7e-39;
0; Mismatches 204; Indels
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                                       9905-0160741.
9905-0160767.
9905-0160767.
9905-0160814.
9905-0160814.
9905-0160981.
9905-0160981.
9905-0161405.
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9905-0161350.
9905-0161350.
9905-0161350.
       99US-0159331.
99US-0159637.
99US-0159638.
99US-0159584.
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                                                                                                                                                                                                                 Best Local Similarity 60.7
Matches 325; Conservative
14-0CT-1999;
14-0CT-1999;
14-0CT-1999;
14-0CT-1999;
18-0CT-1999;
21-0CT-1999;
21-0CT-1999;
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22-0CT-1999;
22-0CT-1999;
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25-0CT-1999;
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25-0CT-1999;
25-0CT-1999;
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26-OCT-1999;
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PR 21-JUN-1999; PR 22-JUN-1999; PR 23-JUN-1999; PR 24-JUN-1999;																																									
ent SEQ ID NO: 59596. apping; gene expressi transduction pathway	ermination s																																								
naliana DNA assay; gene fication; s	<pre>thway; promoter thaliana.</pre>			2000EP-0301439	99US-0121825	99US-0123180. 99US-0123548.	99US-0125788	990S-0120264 990S-0126785	99US-0127462 99US-0128234	990S-0128714	99US-0130077	99US-0130449	99US-0130891	99US-0131449	99US-0132407	99US-0132484	99US-0132486	99US-0132487 99US-0132863	990S-0134256	990S-0134219	99US-0134221 99US-0134370	990S-0134768	990S-0134941 990S-0135124	99US-0135353	990S-0135629 990S-0136021	99US-0136392	990S-0137222	99US-0137528 99US-0137502	990S-0137724	990S-0138094 990S-0138540	99US-0138847	990S-0139452	99US-0139453	99US-0139454	99US-0139455	990S-0139456	99US-0139458	990S-0139459	99US-0139461	990S-0139463.	990S-0139750.
Arabidopsis the Hybridisation protein identification	metabolic pat Arabidopsis t	EP1033405-A2.	06-SEP-2000.	25-FEB-2000;	25-FEB-1999;	05-MAR-1999; 09-MAR-1999;	23-MAR-1999; 25-MAR-1999.	29-MAR-1999;	01-APR-1999; 06-APR-1999;	08-APR-1999;	19-APR-1999;	21-APR-1999; 23-APR-1999;	23-APR-1999;	28-APR-1999;	30-APR-1999;	04-MAY-1999; 05-MAY-1999;	06-MAY-1999;	06-MAY-1999; 07-MAY-1999;	11-MAY-1999;	14 - MAY - 1999;	14-MAY-1999; 14-MAY-1999;	18-MAY-1999;	20-MAY-1999;	21-MAY-1999;	25-MAY-1999;	27-MAY-1999; 28-MAY-1999.	01-JUN-1999;	03-JUN-1999; 04-JUN-1999;	07-JUN-1999;	10-JUN-1999;	10-JUN-1999;	16-JUN-1999;	16-JUN-1999;	18-JUN-1999;	18-JUN-1999;						

990S-0139817990S-0139817990S-0139899990S-0140353990S-0140353990S-0140353990S-0140823990S-0141842990S-0142184990S-0142184990S-0142390990S-0142390990S-0144335990S-0144335990S-0144335990S-0144335990S-0144335990S-0144335990S-0144335990S-0144335990S-0144335990S-0145089990S-0145089990S-0145089990S-0145089990S-0145089990S-0145089990S-0145089990S-0145089990S-0145089990S-0145089990S-0145089990S-0145089990S-0145089990S-0145089990S-0145089990S-0145913990S-0147303990S-0147303990S-0147303990S-0147303990S-0147303990S-0147303990S-0147303990S-0147303990S-0147303990S-0147303990S-0147303990S-0147303990S-0147303990S-0147303990S-0147303990S-0149368990S-0149368990S-0149203990S-0149303990S-0149303990S-0149303990S-0149303-

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useful
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/product= "Arabidopsis thaliana transcription factor"
                             404 accgggaaggataaggagatetteaaaggeaaaggttgtetegttgggatgaagaaaaa 463
                                                                         ttccgtctccaaggatctcatcatcctccaatcattctctgagctctccaaaggaagac 574
                                                                                                                               524 tatcgicitigaaggcaaatattcgtattacaatc---tcccaaaatctgcaagggacgaa 580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence is a cDNA encoding Arabidopsis thaliana transcription factor. This novel transcription factor is useful for modifying a plant's phenotype in desirable ways, such as modifying a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Creelman R, Riechmann JL, Heard J, Ratcliffe O;
                                                                                                                                                                                                                                                                                                                                                  Transcription factor; environmental stress tolerance; gene therapy; plant structure; plant development; ss.
                                                        ttggttttctatcaaggtcgagetcctcgaggccgtaaaaccgattgggtcatgcacgaa
        398 accggcaaagacagaaccattctaaga---aaggggtaagctagttgggatgaggaagaca
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                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana transcription factor G526 cDNA.
                                                                                                                                                           tgggtcttgtgtagggtattccataagaata 605
                                                                                                                                                                        Claim 4; Page 75-76; 116pp; English.
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181..1188
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                                                                                                                                                                                                                                                  AAD06453 standard; cDNA; 1481 BP
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17-APR-2000; 2000US-0197899.
22-AUG-2000; 2000US-0227439.
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(RATC/) RATCLIFFE
(REUB/) REUBER L.
(KEDD/) KEDDIE J.
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(CREE/) C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9; Gaps
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Pred. No. 6.3e-38;
0; Mismatches 182; Indels 9;
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990S-0160981.
990S-0161404.
990S-0161405.
990S-0161359.
990S-0161359.
990S-0161360.
990S-0161361.
990S-0161361.
990S-0161920.
          99US-0151303.
99US-0151438.
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990S-0154018.
990S-0154039.
990S-0154779.
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62.6%;
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99US-0159637.
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99US-0156596
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21-0CT-1999;
22-0CT-1999;
22-0CT-1999;
25-0CT-1999;
25-0CT-1999;
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14-0CT-1999;
14-0CT-1999;
14-0CT-1999;
14-0CT-1999;
18-0CT-1999;
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15-SEP-1999;
16-SEP-1999;
20-SEP-1999;
22-SEP-1999;
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06-0CT-1999;
07-0CT-1999;
12-0CT-1999;
13-0CT-1999;
13-0CT-1999;
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26-OCT-1999;
26-OCT-1999;
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24.5EP-1999;
28.5EP-1999;
29.5EP-1999;
04.0CT-1999;
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21-OCT-1999;
27-AUG-1999;
30-AUG-1999;
31-AUG-1999;
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plants environmental stress. The transcription factor is encoded by environmental stress tolerance gene derived from Arabidopsis thaliana. The transcription factors and the genes encoding them are used to alter soybean, wheat, corn, potato, cotton, rice, oilseed rape, sunflower, alfalfa, sugarcane, tuff, banana, blackberry, blubberry, strawberry, raspberry, cantaloupe, carrot, cauliflower, coffee, onlon, cucumber, peppers, pincapple, spinach, squash, sweet corn, tobacco, tomato, watermelon, rosaceous fruits and/or vegetable brassicas. These sequences are also used for modifying traits associated with environmental stress tolerance, such as freezing, chilling, heat, drought, water saturation, are used in gene therapy.
                                                                                                                                                                                                                                                                     gaagaagagatgaaggaaagtagtataagcatggtggaggcaaagttgcctccgggattc 157
                                                                                                                                                                                                                                                                                                  256 aggittcatccaacagacgaagagatcataacatgitaccitaag---gagaaggitita 312
                                                                                                                                                                                                                                                                                                                                               aataatcatcgaccacctcttgtcctgatccaagtcgatctcaacaagtgtgagccttgg 277
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                                                                                                                                                                          Sequence 1481 BP; 475 A; 266 C; 310 G; 430 T; 0 other;
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99US-0140991
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Arabidopsis thaliana.
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09-MAR-1999

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29-MAR-1999

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                                        568 aaaaccaactgggtgatgcatgagtacaggcttgaagga---aaattctctgcccataac 624
                                                                                                                                                                                                                                                                                       Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
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990S-0125788.
990S-0126785.
990S-012874.
990S-012874.
990S-0130077.
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05-MAR-1999;
23-MAR-1999;
25-MAR-1999;
25-MAR-1999;
06-APR-1999;
06-APR-1999;
16-APR-1999;
16-APR-1999;
23-APR-1999;
23-APR-1999;
23-APR-1999;
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                    209
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                                99US-0148319.
99US-0148341.
99US-0148565.
                                                                                                                                                          99US-0149723.
99US-0149929.
99US-0149902.
                                                                                                                                                                                                       99US-0149930.
99US-0150566.
99US-0150884.
                                                                                                                                                                                                                                                                                                   99US-0151303.
99US-0151438.
99US-0151930.
99US-0152363.
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99US-0154018.
99US-0154039.
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99US-0155139.
99US-0155486.
99US-0155659.
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990S-0160768
990S-0160770.
990S-0160814.
990S-0160815.
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99US-0151066.
99US-0151080.
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990S-0157865.
990S-0158029.
990S-0158232.
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990S-0160989.
990S-0161404.
99US-0161406.
99US-0161359.
99US-0161360.
99US-0161360.
99US-0161363.
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99US-0159293.
99US-0159294.
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99US-0159637.
99US-0159638.
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99US-0149175
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99US-0157117
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99US-0159330
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                                                                               99US-0148684
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09-AUG-1999
11-AUG-1999
11-AUG
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Matches 296;
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3

Gaps

9

Indels

Mismatches

; 0

Conservative

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131 gtggaggcaaagttgcctccgggattcagatttcacccgaaggacgatgagcttgtctgc 190

Page 19

99005-0145086. 99015-0145088. 99015-0145087. 99015-0145087. 99015-0145087. 99015-0145192. 99015-01451182. 99015-0145218. 99015-0145218. 99015-0145218. 99015-0145218. 99015-0145218. 99015-0145218. 99015-0145218. 99015-0145218. 99015-0145218. 99015-0145218. 99015-0145218. 99015-0145218. 99015-0146388. 99015-0147303. 99015-0147303. 99015-0149328. 99015-0149328. 99015-0149929. 99015-0149929. 99015-0149930. 99015-0149930. 99015-0149930. 99015-0151066. 99015-0151066. 99015-0151066. 99015-0151066. 99015-0151066. 99015-0151066. 99015-0151066. 99015-0151066. 99015-0151066. 99015-0151066. 99015-0151066. 99015-0151066.	9905-0158029. 9905-0158232. 9905-0158232. 9905-0159294. 9905-0159295. 9905-0159330. 9905-0159331.
21-JUL-1999; 22-JUL-1999; 22-JUL-1999; 22-JUL-1999; 23-JUL-1999; 23-JUL-1999; 23-JUL-1999; 27-JUL-1999; 27-JUL-1999; 27-JUL-1999; 28-JUL-1999; 28-JUL-1999; 28-JUL-1999; 28-JUL-1999; 28-JUL-1999; 28-JUL-1999; 28-JUL-1999; 38-JUL-1999; 38-JU	7 - OCT 1999; 8 - OCT 1999; 3 - OCT 1999; 3 - OCT 1999; 4 - OCT 1999; 4 - OCT 1999; 4 - OCT 1999; 6 - OCT 1999; 7 - OCT 1999; 8 - OCT 1999;
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905-0132048 905-0132407. 905-0132486. 905-0132487. 905-0132487. 905-0132487. 905-0132487. 905-0134218. 905-0134218. 905-0134218. 905-0134218. 905-0134218. 905-0134218. 905-0134218. 905-0134218. 905-013494. 905-013522. 905-013522. 905-0137522. 905-013945. 905-014035.	0-S06 0-S06 0-S06 0-S06 0-S06 0-S06 0-S06 0-S06 0-S06 0-S06 0-S06
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metabolic pathway; promoter; termination sequence;
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990S - 0.136021

990S - 0.136322

990S - 0.13722

990S - 0.13728

990S - 0.13724

990S - 0.13945

990S - 0.13945
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99US-0126785.
99US-0127462.
99US-0128234.
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99US-0129845.
99US-0130047.
99US-0130891.
99US-0131449.
99US-0131449.
99US-0132407.
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99US-0139461.
99US-0139462.
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99US-0139750.
99US-0139763.
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99US-0140695
                                     Arabidopsis thaliana
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06-MAY-1999;

07-MAY-1999;

07-MAY-1999;

11-MAY-1999;

14-MAY-1999;

14-MAY-1999;

14-MAY-1999;

14-MAY-1999;

14-MAY-1999;
                                                                   EP1033405-A2
                                                                                                                                                           25-FEB-1999;
05-MAR-1999;
09-MAR-1999;
23-MAR-1999;
25-MAR-1999;
01-APR-1999;
06-APR-1999;
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20-MAY-1999;
21-MAY-1999;
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25-MAY-1999;
27-MAY-1999;
28-MAY-1999;
01-JUN-1999;
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19-APR-1999;
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23-APR-1999;
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28-APR-1999;
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18-JUN-1999;
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        5
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                                                                                                                                                                                                                                                                                                                                                                                                                                        191 gattacttgatgagacgatcgcttcacaataatcatcgaccacctcttgtcctgatccaa 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     371 gcaacggccaccggatattggaaagccaccggcaaagacagaaccattctaagaaagggt 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               209 gagcagatggatttacctcctgggttcaggtttcatccaacagatgaagaactcataact 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gattggtatttctacagccaaagagccgaaaatacgcgacgggggtgagaactaaccga 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              386 gaatggtattttttttgtgtgagagacagaaagtatcccaccggtttaagaactaaccga 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         431 aagctagttgggatgaggaagacattggttttctatcaaggtcgagctcctcgaggccgt 490
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          446 gcaactgaagccggttattggaaggcgaccgggaaggataaagagatataccgaggcaaa
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                                                                                                                                                                                                                                                                                                                   Length 1355;
                                                                                                                                                                                                                                                                                                                12.6%; Score 162; DB 21; Length 1 61.4%; Pred. No. 3.6e-35; ive 0; Mismatches 180; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis thaliana DNA fragment SEQ ID NO: 29918.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAC40896 standard; DNA; 1358 BP.
 99US-0160741.
99US-0160767.
99US-0160768.
99US-0160814.
99US-0160815.
                                                                                                                                                                                                                     990S-0161361.
990S-0161920.
990S-0161992.
990S-0161993.
                                                                                                            99US-0160981.
99US-0160989.
99US-0161404.
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99US-0161406.
99US-0161359.
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21-0CT-1999;
21-0CT-1999;
21-0CT-1999;
21-0CT-1999;
22-0CT-1999;
22-0CT-1999;
25-0CT-1999;
25-0CT-1999;
26-0CT-1999;
26-0CT-1999;
26-0CT-1999;
28-0CT-1999;
28-0CT-1999;
28-0CT-1999;
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683 gg 684
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giggaggcaaagtigcciccgggaticagatitcacccgaaggacgaigagctigtcigc 190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 160; DB 21; Length 13
Pred. No. 1.3e-34;
0; Mismatches 180; Indels
                                                                                                                                                                                                                                                                                          990S-0160768
990S-0160770
990S-0160814
990S-0160818
990S-0160980
990S-0160989
990S-0161405
990S-0161405
990S-0161350
990S-0161350
990S-0161350
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61.2%;
          990S - 0153758
990S - 0153758
990S - 0154779
990S - 0154779
990S - 0155486
990S - 0155586
990S - 0155596
990S - 0157717
990S - 0157753
990S - 0157753
990S - 0159785
990S - 0159785
990S - 0159785
990S - 0159295
990S - 0159295
990S - 0159295
990S - 0159330
990S - 0159330
990S - 0159330
990S - 0159331
990S - 0159331
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99US-0161993.
99US-0162142.
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Best Local Similarity 61.2
Matches 295; Conservative
10.SEP-1999;

15.SEP-1999;

16.SEP-1999;

20.SEP-1999;

22.SEP-1999;

24.SEP-1999;

24.SEP-1999;

25.SEP-1999;

26.OCT-1999;

26.OCT-1999;

27.SEP-1999;

28.SEP-1999;

28.SEP-1999;

29.SEP-1999;

20.OCT-1999;

21.OCT-1999;

21.OCT-1999;

22.OCT-1999;

23.OCT-1999;

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26.OCT-1999;

27.OCT-1999;

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28.OCT-1999;

28.OCT-1999;
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990S - 0140823.
990S - 0141842.
990S - 0141842.
990S - 0142154.
990S - 0142365.
990S - 0142390.
990S - 0142970.
990S - 0142970.
990S - 014400S.
990S - 01444085.
990S - 01444332.
990S - 0144333.
990S - 0144333.
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99US-0145086.
99US-0145088.
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990S-0145087
990S-0145192.
990S-0145145.
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transcription factor homologue. This novel transcription factor transcription factor homologue. This novel transcription factor decided to a setul for modifying a plant's phenotype in desirable ways, such as encoded by environmental stress. The transcription factor is encoded by environmental stress. The transcription factor is encoded by environmental stress tolerance gene derived from Arabidopsis thaliana. The transcription factors and the genes encoding them are used to alter the structure and developmental characteristics of plants such as soybean, wheat, corn, potato, cotton, rice, oilseed rape, sunflower, alfalfa, sugarcane, turf, banana, blackberry, papaya, strawberry, raspberry, cantaloupe, carrot, calliflower, coffee, onlon, cucumber, eggplant, grapes, honey dew, lettuce, mango, melon, blueberry, peas, peppers, pineapple, spinach, squash, sweet corn, tobacco, tomato, watermelon, rosaceous fruits and/or vegetable brassicas. These sequences care also used for modifying traits associated with environmental stress tolerance, such as freezing, chilling, heat, drought, water saturation, calt, photoconditions, radiation and ozone. The transcription factors
                                                                                                                                                                                                                                                             Nucleic acids encoding plant transcription factor polypeptides, useful for altering the environmental stress tolerance characteristics of
                                                                                                                          Yu G, Creelman R, Riechmann JL, Heard J, Ratcliffe O;
Keddie J;
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RIECHMANN J L.
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                                                          (REDD/) REDDIE J. (KEDD/) KEDDIE J.
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Maximum DB seq length: 200000000
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Match Length DB
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Sequence 122,
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
US-09-372-422A-39
US-09-439-313-353
US-09-972-422A-35
US-08-64459-1
US-09-001-273-1
US-08-84459A-1
US-09-061-400-1
US-09-061-400-1
US-08-446-855A-1
US-08-157-309B-22
US-08-857-309B-22
US-08-834-306-22
US-08-933-674A-2
US-08-931-3300-6
US-08-913-300-6
US-08-950-720A-5
US-09-248-335-472
US-09-248-335-472
US-09-248-335-472
                                                                                                                                                                                                                                                                          Sequence 14, Application US/08232463
Sequence 14, Application US/08232463
Patent No. 5670367
SPATEMAL INFORMATION:
APPLICANT: SCHEIFLINGER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
ITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 30472/114 IMMU TELECOMMUNICATION: TELEPHONE: (703)836-9300
                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 1800 Diagonal Road, Suite 500 CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: EP 91 114 300.6 FILING DATE: 26-AUG-1991 ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/07/935,313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                 Foley & Lardner
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INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7218 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: BENT, Stephen A. REGISTRATION NUMBER: 2
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MEDIUM TYPE: Floppy
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
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ZIP: 22313-0299
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Query Match
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                                                                                                                                                                                                                                                 168 cgaaggacgatgagcttgtctgcgattacttgatgagacgatcgcttcacaataatcatc 227
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                                                                                                                                                                 108 tgaaggaaagtagtataagcatggtggaggcaaagttgcctccgggattcagatttcacc 167
                                                                                  48 ctaatcaaacactaaaacctagaaaaaaaaagatcaaatcatggagacggaagaagaga 107
                                           0; Gaps
ch 4.4%; Score 57; DB 1; Length 7218; 1 Similarity 9.1%; Pred. No. 3.5e-07; 42; Conservative 223; Mismatches 198; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1051 GACCTGCAGCCCAAGCTCGGAATTAATTCTGTGAGCGTATGGCA 1009
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALSKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
MUMBER OF SEQUENCES: 52
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F: 1800 Diagonal Road, Suite 500
Alexandria
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
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ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 3047
TELECOMMUNICATION INFORMATION:
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IBM PC compatible
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      Query Match 4.4%;
Best Local Similarity 9.1%;
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ADDRESSEE: Foley & L
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC
OPERATING SYSTEM:
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US-08-232-463-14
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HUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E: SmithKline Beecham Corporation 709 Swedeland Road
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FILING DATE: 04-FEB-1997
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/08794796 Patent No. 5885800
              TELEFAX: (703)663-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACIERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
(703)836-9300
                                                                                     7218 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Emery, John
APPLICANT: Trun, KB
APPLICANT: Trunch, Alem
APPLICANT: Young, Peter
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                                                                                                                       single
                                                                                                      nucleic acid
                                                                                                                                                                   US-08-232-463-14
                                                                                                                                         linear
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                                                                                                                                       TOPOLOGY: line
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                                                                                                      TYPE: nucleic
STRANDEDNESS:
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 TELEPHONE:
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CORRESPONDENCE ADDRESS:
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STATE: California
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LOCATION: 117
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APPLICANT: Mandall, Douglas D.
APPLICANT: Mandall, Douglas D.
APPLICANT: Maiernyk, Jan A.
APPLICANT: Mernyk, Jan A.
APPLICANT: Mernyk, Michael H.
APPLICANT: Menchy, Michael H.
APPLICANT: Meoney, Brian P.
TITLE OF INVENTION: GES OF DNA ENCODING PLASTID PYRUVATE DEHYDROGENASE AND TITLE OF INVENTION: BRANCHED CHAIN OXOACID DEHYDROGENASE COMPONENTS TO TITLE OF INVENTION: ENHANCE POLYHYDROXALKANOATE BIOSYNTHESIS IN PLANTS FILE REFERENCE: UMO 1482
CURRENT APPLICATION NUMBER: US/09/108,020A
CURRENT FILING DATE: 1997-06-30
EARLIER FILING DATE: 1997-06-30
SEARLIER FILING DATE: 1997-06-30
SOFWMARE: PAPLICATION NUMBER: 6//076,544
EARLIER FILING DATE: 1998-03-02
SOFWMARE: PATENTING DATE: 1998-03-02
SOFWMARE: PATENTIN VEY: 2.1
SSOF ID NOS: 54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
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                                                                                   GH50000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/09108020A Patent No. 6143561
GENERAL INFORMATION:
                                   NAME: Han, William T
REGISTRATION NUMBER: 34,344
REFRENCE/DOCKET NUMBER: GH50
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5219
TELEFAX: 610-270-4026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-108-020-1
                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 3.1%;
Best Local Similarity 56.6%;
Matches 73; Conservative (
                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1164 base pairs
                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                   ; MOLECULE TYPE: CDNA
US-08-794-796-1
                                                                                                                                                                                                                                                                                                        linear
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FILING DATE:
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US-09-108-020-1
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1154 gtacaaacatttcctcactcttgtacccacggtagattcatgtaaaataccacttatgac 1213

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                                                                                        APPLICANT: Seghezzi, Wolfgang
APPLICANT: Shanaban, Frances
APPLICANT: Lees, Emma M.
APPLICANT: McClanahan, Terrill K.
APPLICANT: McClanahan, Terrill K.
TITLE OF INVENTION: Intracellular Regulatory Molecules;
TITLE OF INVENTION: Related Reagents
NUMBER OF SEQUENCES: 13
                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/OR/Annormal
                                                                                                                                                                                                                                                                      3: DNAX Research Institute
901 California Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/032,818
FILING DATE: 11-DEC-1996
ATTORNEY/AGENT INFORMATION:
Sequence 1, Application US/08999774A Patent No. 6274312
                                            GENERAL INFORMATION:
APPLICANT: Gish, Kurt C.
APPLICANT: Seghezzi, Wolfgang
APPLICANT: Shanahan, Frances
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34,090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: (650)852-9196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                            ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 4081 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (650)496-1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Ching, Edwin P. REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1279 ggcggccgc 1287
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                      ; Sequence 50, Application US/09232201A
; Patent No. 6348321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 7, Application US/08713000
; Patent No. 5850020
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ATTORNEY/AGENT INFORMATION:
NAME: Sleath, Janet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Seattle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 98121
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                                                                                                                                                                 US-09-232-201-50
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US-08-713-000-7
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85.4%; Pred. No. 0.18;
tive 0; Mismatches 7; Indels 0;
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                                                                                                                                                                                      APPLICANT: Stahl, Andreas
APPLICANT: Stahl, Andreas
APPLICANT: Hirsch, David J.
APPLICANT: Glucish, Harvey F.
APPLICANT: Glucon, Ruth E.
APPLICANT: Glucon, Ruth E.
APPLICANT: Tartaglia, Louis A.
TITLE OF INVENTION: FATTY ACID TRANSPORT PROTEINS
FILE REERENCE: WHIST-21p3MB
CURRENT APPLICATION WUMBER: US/09/232,200A
CURRENT APPLICATION WUMBER: 60/071,374
EARLIER FILING DATE: 1998-01-14
EARLIER APPLICATION WUMBER: 60/03,491
EARLIER APPLICATION NUMBER: 60/03,491
EARLIER APPLICATION NUMBER: 60/03,491
EARLIER APPLICATION NUMBER: 60/10,941
EARLIER FILING DATE: 1998-07-20
EARLIER FILING DATE: 1998-12-04
NUMBER OF SEQ ID NOS: 105
SUFWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 50. Application US/09232197A

Sequence 50. Application US/09232197A

GENERAL INFORMATION:
APPLICANT: Stahl, Andreas
APPLICANT: Hirsch, David J.
APPLICANT: Gimeno, Ruth E.
APPLICANT: Gimeno, Ruth E.
TITLE OF INVENTION: FATTY ACID TRANSPORT PROTEINS
FILE REFERENCE: WH197-21p3MA
CURRENT APPLICATION NUMBER: US/09/232,197A
CURRENT FILING DATE: 1999-01-14
EARLIER FILING DATE: 1998-01-15
EARLIER APPLICATION NUMBER: 60/011,374
EARLIER FILING DATE: 1998-01-15
EARLIER APPLICATION NUMBER: 60/03,491
EARLIER FILING DATE: 1998-07-20
EARLIER FILING DATE: 1998-07-20
EARLIER FILING DATE: 1998-12-04
NUMBER OF SEQ ID NOS: 105
SOFTWARE: FASTSEQ for Windows Version 3.0
                                                                                           US-09-232-200-50
; Sequence 50, Application US/09232200A
: Datent No. 6288213
; GENERAL INFORMATION:
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Best Local Similarity 85.4.
Best Local 1; Conservative
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; ORGANISM: Homo sapiens
US-09-232-200-50
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US-09-232-197-50
4073 GGCGGCCGC 4081
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LENGTH: 1173
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APPLICANT: Havukkala, Ilkka
APPLICANT: Havukkala, Ilkka
APPLICANT: Havukkala, Ilkka
APPLICANT: Havukkala, Ilkka
TITLE OF INVENTION: MATERIALS AND METHODS FOR THE
TITLE OF INVENTION: MODIFICATION OF PLANT LIGNIN CONTENT
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: 2601 Elliott Avenue, Suite 4185
                                                                                                                                                                                                                                                                             APPLICANT: Stahl, Andreas
APPLICANT: Hirsch, David J.
APPLICANT: Hirsch, David J.
APPLICANT: Lodish, Harvey F.
APPLICANT: Codish, Harvey F.
APPLICANT: Gimeno, Ruth E.
TITLE OF INVENTION: FATTY ACID TRANSPORT PROTEINS
FILE REFERENCE: WHI97-21p3M
CURRENT FILING DATE: 1999-01-14
EARLIER APPLICATION NUMBER: 60/071,374
EARLIER PILING DATE: 1998-01-15
EARLIER PILING DATE: 1998-01-15
EARLIER FILING DATE: 1998-07-20
EARLIER PILING DATE: 1998-07-20
EARLIER PILING DATE: 1998-07-20
EARLIER FILING DATE: 1998-12-04
NUMBER OF SEQ ID NOS: 105
SSOFTWARE: FASTSEQ FOR WINDOWS VERSION 3.0
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APPLICATION NUMBER: US/08/713,000
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GENERAL INFORMATION:
APPLICANT: Bloksberg, Leonard N.
APPLICANT: Bloksberg, Leonard N.
APPLICANT: Bloksberg, Leonard N.
APPLICANT: Grierson, Alastair
TITLE OF INVENTION: Materials and Methods for the
TITLE OF INVENTION: Modification of Plant Lignin Content;
FILE REFERENCE: 11000.100323
CURRENT APPLICATION NUMBER: US/09/211,710A
CURRENT FILING DATE: 1998-12-14
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 7
LENGTH: 1454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/975,316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Ann W. Speckman
STREET: 2601 Elliott Avenue, Suite 4185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11000/1003C1
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APPLICATION NUMBER: 08/713,000
FILING DATE: September 11, 1996
ATTORNEY/AGEN: INFORMATION:
NAME: SLEATH, Janet
REGISTRATION NUMBER: 37,007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 71, Application US/08975316 Patent No. 5952486 GENERAL INFORMATION:
                                                                                                                                        Sequence 7, Application US/09211710A Patent No. 6204434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: 206-269-0565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 2.85
Best Local Similarity 76.35
Matches 45; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          206-269-0563
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Pinus radiata US-09-211-710-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 2601 ECITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
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Patent No. 5952486
GENERAL INFORMATION:
APPLICANT: BLOKSBERG, Leonard N., HAVUKKALA, Ilkka
APPLICANT: and GRIERSON, Alastair W.
TITLE OF INVENTION: THE MODIFICATION OF PLANT LIGNIN CONTENT
NUMBER OF SEQUENCES: 88
                                                                                                                                                                                                                                                                                    2.8%; Score 36.6; DB 2; Length 1454; 76.3%; Pred. No. 0.24; tive 0; Mismatches 14; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1454;
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Pred. No. 0.24;
0; Mismatches 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Ann W. Speckman STREET: 2601 Elliott Avenue, Suite 4185 CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/975,316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/713,000
FILING DATE: September 11, 1996
ATTORNEY/AGBNT INFORMATION:
NAME: SLEATH, Janet.
REGISTRATION NUMBER: 37,007
REPERENCE/DOCKET NUMBER: 11000/1003C1
TELECOMUNICATION INFORMATION:
TELEPHONE: 206-269-0565
                   11000.1003
                   REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-269-0565
REGISTRATION NUMBER: 37,007
                                                                                              INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1454 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 1454 base pairs
TYPE: nucleic acid
                                            TELEPHONE: 206-20563
                                                                                                                                                                                                                                                                                                                              45; Conservative
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Best Local Similarity 76.3
Matches 45; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 206-269-0563
                                                                                                                                                                                   single
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CLASSIFICATION: 800
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US-08-975-316-7
                                                                                                                                                                                                    TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                         Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
                                                                                                                                                                               STRANDEDNESS:
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US-08-975-316-7
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APPLICANT: and GRIEBSON, Alastair W.
TITLE OF INVENTION: MATERIALS AND METHODS FOR
NUMBER OF SEQUENCES: 88
                                                                                                                                                                                                                                                                                                                                                                                                       Score 36.6; DB 4; Length 1454;
Pred. No. 0.24;
0; Mismatches 14; Indels 0
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us-09-889-926-1.rni

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2.7%; Score 35.2; DB 1; Length 684; 58.1%; Pred. No. 0.42;
            TITLE OF INVENTION: PRODUCTION OF RECOMBINANT FACTOR XA TITLE OF INVENTION: INHIBITORS OF LEECH HIRUDO MEDICINALIS NUMBER OF SEQUENCES: 28 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 36, Application US/09232200A

Patent NO. 6288213

GENERAL INFORMATION:
APPLICANT: Stall, Andreas
APPLICANT: Hirsch, David J.
APPLICANT: Gineno, Ruth E.
APPLICANT: Tartaglia, Louis A.
TITLE OF INVENTION: FATTY ACID TRANSPORT PROTEINS
FILE REPERENCE: WHIF97-21p3MB.
CURRENT APPLICATION NUMBER: US/09/232,200A
                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
APPLICATION NAMBER: US/08/226,264
FILING DATE: 08-APR-94
                                                                                                                                                                                                                                                                                                                                             AFFLICAL:
AFFLICATION: 630
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: White, John P. 28,678
REGISTRATION NUMBER: 28,678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                             ADDRESSEE: Cooper & Dunham LLP STREET: 1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT FILING DATE: 1999-01-14
EARLIER APPLICATION NUMBER: 60/011,374
EARLIER APPLICATION NUMBER: 60/01374
EARLIER APPLICATION NUMBER: 60/093,491
EARLIER FILING DATE: 1998-07-20
EARLIER FILING DATE: 1998-07-20
EARLIER FILING DATE: 1998-12-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 40C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   68.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 684 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
APPLICANT: Fischer, Meir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 2.74
Best Local Similarity 68.15
Matches 49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 212-391-0525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1266 aaaaaaaaaaa 1277
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                                                                                                                                  CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ANTI-SENSE: NO US-08-226-264-27
                                                                                                                                                                           COUNTRY: U. ZIP: 10036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HYPOTHETICAL:
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US-09-232-200-36
                                                                                                                                                           STATE:
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                                                                                                                                                                                                                                                            Gaps
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0
                                                                                                                                                                             Score 36.6; DB 2; Length 1474; Pred. No. 0.24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2.8%; Score 36.4; DB 4; Length 611; 66.7%; Pred. No. 0.17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
TITLE OF INVENTION: PRODUCTS: II
FILE REFERENCE: CCDNA-260XX
CURRENT APPLICATION NUMBER: US/09/385,982
CURRENT FILING DATE: 1999-06-08
EARLIER APPLICATION NUMBER: 09/328,111
EARLIER APPLICATION NUMBER: 60/117,393
EARLIER FILING DATE: 1999-01-07
EARLIER FILING DATE: 1999-01-07
EARLIER FILING DATE: 1999-031
NUMBER OF SEQ ID NOS: 544
SEQ ID NO 376
SEQ ID NO 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26; Indels
                                                                                                                                                                                                                   14; Indels
                                                                                                                                                     Query Match 2.8%; Score 36.0; Local Similarity 76.3%; Pred. No. 0.24; Best Local Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                          US-09-385-982-376; Sequence 376, Application US/09385982; Patent No. 6262334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 27, Application US/08226264 Patent No. 5801017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; LOCATION: (1)...(611)
; OTHER INFORMATION: n = A,T,C or G
US-09-385-982-376
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Zeelon, Elisha P.
Levanon, Avigdor
Guy, Rachel
Goldiust, Arie
Rigbi, Meir
Panet, Amos
INFORMATION FOR SEQ ID NO: 71:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1260 aaaaaaaaaaaaaaaa 1277
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                                 LENGTH: 1474 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens
                                                                                               ; TOPOLOGY: linear
US-08-975-316-71
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APPLICANT:
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

(without alignments) 1752.981 Million cell updates/sec July 15, 2002, 06:55:13; Search time 17.76 Seconds Run on:

US-09-889-926-2 1757 1 METEEEMKESSISMVEAKLP......BGSSESLLTDIGIPSTVWNC 324 Perfect score: Title:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Sequence:

283138 seqs, 96089334 residues Searched:

283138 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Maximum Match 100% Listing first 45 summaries Post-processing: Minimum Match 0%

PIR\_71:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		de			SOMERIES	
Result		Query				
No.	Score	Match	Length	DB	ID	Description
1	1579.5	89.9	309	7	C96601	hypothetical prote
7	536.5	30.5	334	7	н96791	unknown protein Fl
e	505.5	28.8	316	~	E84636	NAM (no apical mer
4	491.5	28.0	365	7	G84559	
2	473	26.9	298	7	н96584	
9	472.5	26.9	334	7	T47983	+
7	470.5	26.8	324	7	B96742	NAM-like protein,
80	459.5	26.2	399	7	T02678	NAM (no apical mer
6	456	26.0	377	ď	T04585	hypothetical prote
10	456	26.0	418	N	E86395	
11	453.5	25.8	631	~	D96683	
12	446.5	25.4	341	7	T04050	
13	439	25.0	320	7	A96570	NAM-like protein,
14	438.5	25.0	358	~	E86452	protein F6N18.15 [
15	436.5	24.8	317	7	B96570	NAM-like protein,
16	436	24.8	300	~	н96636	hypothetical prote
17	436	24.8	314	N	T08933	
18	436	24.8	409	N	G86257	
19	434	24.7	305	7	F86456	unknown protein [i
20	429	24.4	253	7	696803	GRAB1-like protein
21	423.5	24.1	303	~	T52345	OsNAC6 protein [im
22	421	24.0	289	7	E86148	TlN6.12 protein -
23	$\sim$	23.9	329	~	T52344	-OsNAC5 protein [im
24	413.5	23.5	534	~	T04663	hypothetical prote
25	411	23.4	268	~	T52343	hypothetical prote
56	410.5	23.4	267	7	T48437	
27	397.5	22.6	275	7	G84860	NAM (no apical mer
28	S)	22.5	262	~	T05084	hypothetical prote
29	390.5	22.2	268	~	A84746	probable NAM (no a

hypothetical prote	hypothetical prote	hypothetical prote	NAM (no apical mer	NAM (no apical mer	NAM (no apical mer	hypothetical prote	BTF3b factor prote	NAC2-like protein	hypothetical prote	CDS protein F9L11.	ATAF2 protein - Ar	NAC-domain protein	ATAF1 protein - Ar	probable NAM-like	hypothetical prote
T04624	F86450	T07182	D84547	G84436	C84671	B86466	A86466	T46230	T49145	E86453	S37100	T52342	S37101	B85020	T01942
7	~	7	7	~	7	7	7	7	7	7	~	7	7	7	7
315	283	272	276	176	335	557	216	469	332	522	220	229	229	457	302
			~	_										'n	
21.5	21.3	21.1	20.8	20.7	20.6	20.6	20.4	19.8	19.1	18.6	17.6	16.6	16.1	15.	14.5
	374 21.3							347.5 19.8						273.5 15.0	

## ALIGNMENTS

RESULT 1 (9660)  hypothatical protects meusy 10 (immorted) - Arabidoneis thalians
"Ypochecical process arabidopsis thaliana (mouse-ear cress)
C;Date: UZ-Mar-ZUUI #sequence_revision UZ-Mar-ZUUI #text_change 31-Mar-ZUUI C;Accession: C96601
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon Chin, C.W.; Chunq, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,
ansen, N.F.; Hughes, B.; Huizar, L. Nature 408, 816-820, 2000
A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A; Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719
A; Accession: C96601
A;Status: preliminary
A; Molecule type: DNA
A; Residues: 1-309 <sto></sto>
A; Cross-references: GB: AE005173; NID: q6056383; PIDN: AAF02847.1; GSPDB: GN00141
C;Genetics:
A;Gene: T6H22.19
A; Map position: 1

Gaps Indels 25; 89.9%; Score 1579.5; DB 2; Length 309; 91.8%; Pred. No. 1.9e-129; Live 0; Mismatches 2; Indels 25; Query Match 89.9 Best Local Similarity 91.8 Matches 302; Conservative

3;

61 EPWDIP----KMACVGGKDWYFYSQRDRKYATGLRTNRATATGYWKATGKDRTLLRKGK 115 116 LVGMRKTLVFYQGRAPRGRKTDWVMHEFRLQGSHHPPNHSLSSPKEDWVLCRVFHKNTEG 175 176 VICRDNMGSCFDETASASLPPLMDPYINFDQEPSSYLSDDHHYIINEHVPCFSNLSQNQT 235 g δλ g δy g δŏ Qγ

236 LNSNLTNSVSELKIPCKNPNPLFTGGSASATLTGLDSFCSSDQMVLRALLSQLTKIDGSL 295 οp δ

296 GPKESQSYGEGSSESLLTDIGIPSTVWNC 324 qq δ

Mon Jul

11;

Gaps

73;

Length 316;

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Cydrosesion: G84559
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y
M.; Koo, H.; Moffat, K.S.; Cronli, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon,
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID: 20083487
A;Accession: G84559
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-365 <STO>
A;Cross.references: GB:AE002093; NID: 94406812; PIDN:AAD20120.1; GSPDB:GN00139
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          probable NAM (no apical meristem)-like protein [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
  76 WYFYSQRDRKYATGLRTNRATATGYWKATGKDRTILRK--GKLVGMRKTLVFYQGRAPRG 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        72 WYFFSLRDKKYPTGVRTNRATNTGYWKTTGKDKEIFNSTTSELVGMKKTLVFYRGRAPRG 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               132 EKTCWVMHEYRL----HSKSSYRTSKODEWVVCRVFKKTEATKKYISTSSSSTSHHHNNH 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SDDHHYIIN-EHVPCFSNLSQNQTLNSNLTNSVSELKIPCKNPNPLFT---GGSASATLT 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      248 DSSHQQLMNYTHMPV-----SGLNLNLGGALVQ-----PPPVVSLEDVAAVSASYN 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          73 --GKDWYFYSQRDRKYATGLRTNRATATGYWKATGKDRTILRKGKLVGMRKTLVFYQGRA 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    131 PRGRKTDWVMHEFRLQGSHHPPNHSLSSPKED-WVLCRVFHKNTEGVICRDNMGSC---F 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 MESCSVPPGFRFHPTDEELV-GYYLRKKIASQKIDLDVIRDIDLYRIEPWDLQEQCRIGY 62
                                                                                                                                                                                                                                                                                                                                                           16 EAKLPPGFRFHPKDDELVCDYLMRRSLHNNHRPPLVLIQVDLNKCEPWDIPKMACVGGKD 75
                                                                                                                                                                                                                                                                                                                                                                                                                   13 EEALPPGFRFHPTDEELISYYLVNKIADQNFTGK-AIADVDLNKSEPWELPEKAKMGGKE 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14 MVEAKLPPGFRFHPKDDELVCDYLMRRSLHNNHRPPLVLIQVDLNKCEPWDIPKMACVG-
                                                                                                                                                                                                                                                                                                         87; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        91; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2;
                                                                                                                                                                                                                                                 DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       173 TEGVICRDNMGSCFDETASASLPPLMDPY--INFDQ------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          134 RKTDWVMHEFRLQGSHHPPNHSLSSPKEDWVLCRVFHK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28.0%; Score 491.5; DB 2 38.4%; Pred. No. 7.1e-35; iive 49; Mismatches 91
                                                                                                                                                                                                                                                 28.8%; Score 505.5; DB 2 36.3%; Pred. No. 3.5e-36;
                                                                                                                                                                                                                                                                                                         47; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 269 GLDSFCSSDQMVLRALLSQLTKIDG 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      294 GENGFGNVE-----MSQCMDLDG 311
                                                                                                                                                                                                                                                                                                            Matches 118; Conservative
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                                                                                                                                                                                                                                                                                 Best Local Similarity
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A;Status: preliminary
                                                                                                                                 A; Gene: At2g24430
A; Map position: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Gene: At2g18060
A; Map position: 2
                                                                                                                                                                                                                                                    Query Match
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Nature 408, 816-820, 2000
A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowney, T.; Sakano, H.
A; Authors: Salzberg, S.L.; Sakano, H. Shina, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A; Hiller, Sequence and analysis of Chromosome 1 of the plant Arabidopsis.
A; Accession: H96791
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R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Kaul, S.; Rounsley, S.D.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, Leuss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Nature, 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11;
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                                                                                                                                                                                            C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Accession: H96791
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WYFYSORDRKYATGLRINRATATGYWKATGKDRIILR--KGKLVGMRKTLVFYOGRAPRG 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   134 RKTDWVMHEFRLQGSHHPPNHSLSSPKEDWVLCRVFHKNTEGVICRDNMGSCFDETA--- 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----SASLPPLMDP----YINFDQEPSSYLSDDHHYIINEHVPCFSNLSQNQT 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19 ERGLPPGFRFHPTDEELITFYLASKIFHGG-LSGIHISEVDLNRCEPWELPEMAKMGERE 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               236 LNSNLTNSVSELKIPCKNPNPLFTGGSASATLTGLDSFCSSDQMVLRALLSQLTKI----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              87;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67; Indels
                                                                                                                                                                 unknown protein F14G6.2 [imported] - Arabidopsis thaliana
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 30.5%; Score 536.5; DB 2
Best Local Similarity 38.3%; Pred. No. 7.8a-39;
Matches 123; Conservative 44; Mismatches 67
281 GPKESQSYGEGSSESLLTDIGIPSTVWNC 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ------DGSLGPKESQS 302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |: : :: |||
236 LHGSSGHNIDELK------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-334 <STO>
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Length 365;

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123 187 177 247 228	A;Reference number: 224481 A;Accession: T47983 A;Status: preliminary A;Molecule type: DNA A;Residues: 1.334 <cho> A;Cross_references: EMBL.AL138642 A;Cross_references: EMBL.AL138642 A;Experimental source: cultivar Columbia; BAC clone F21F14 C;Genetics: A;Map position: 3 A;Introns: 58/1 A;Note: F21F14.80</cho>
<pre>RESULT 5 H96584 hypothetical protein F20D21.15 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001</pre>	ttch 26.9%; Score 472.5; DB 2; Length 334; sal Similarity 33.1%; Pred. No. 2.8e-33; losservative 52; Mismatches 89; Indels 99; Ga
C;Accession: H96584 R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Hużar, L.	QY 16 EAKLPPGFRFHPKDDELVCDYLMRRSLHNNHRPPLVLIQVDLNKCEPWDIPKMACVG 72 ::::        ::  :   : :       :
Nature 408, 816-820, 2000 A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.	QY 73 GKDWYFYSQRDRKYATGLRTNRATATGYWKATGKDRTILRKGKLVGMRKTLVFYQGRAPR 132        : :
A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. A; Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  A: Reference number: ASK141. WITH. 2016.710	Qy 133 GRKTDWVMHEFRLQGSHHPPNHSLSSPKEDWVLCRVFHKNFEGVICRDNM 182  : :  :  :
A; Accession: H96584 A; Status: preliminary A; Molecule type: DNA	QY 183 GSCFDETASASLPPLMDPYINFDQEPSSYLSDDHYIINEH 223
A; Gross-references: GB: AE005173; NID: 94585977; PIDN: AAD25613.1; GSPDB: GN00141 C; Genetics: C; Genetics: A;	QY 224 VPCFSNLSQNQTLNSNLTNSVSELKIPCKNPNPLFTGGSASATLTGLDSFCSSDQM 279 :   :   :     :     :     :       :   Db 227 LECHNNTTITSYQWLIDDQVNNCHVSKVMDPSFITSWAA 265
1 26.9%; Score 473; DB 2 nilarity 40.1%; Pred: No. 2.2e=3	OY 280 VLRALLSOLTKIDGSLGPKESQSYGEGSSESLLTDIGIPS-TWWN 323 :
<pre>Matches 112; Conservative 26; Mismatches 61; Indels 80; Gaps 10; Qy 19 LPPGFRFHPKDDELVCDYLMRRSLHNNHRPPLVLI-QVDLNKCEPWDIPKMACVGGKD 75</pre>	RESULT 7 B96742
	NAM-like protein, 48543-50167 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress)
Qy 76 WYFYSQRDRKYATGLRTNRATATGYWKATGKDRTILRKGKLVGWRKTLVFYGGRAPRGRK 135	C, Accession: B96742 R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.B.; Creasy, T.H.; Dewar,
QY         136 TDWVMHEFRLQGSHHPPNHSLSSPKEDWVLCRVFHKN	ansen, N.F.; Hughes, B.; Hulzar, L. Nature 408, 816-820, 2000 A.Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Malti, R.; Marzia
QY 173TEGVICRDNMGSCFDETASASLPPLMDPYINFDQ 206 :	Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. A.Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. A.; Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
QY 207 EPSSYLSDDHYIINEHVPCFSNLSQNQ 234	A.Reference number: A86141; MUD:21016719 A.Accession: B96742 A.Katus: preliminary A.Molecule type: DNA
RESULT 6 147983 NAM-like protein - Arabidopsis thaliana	A.Residues: 1-324 <sto> A.Cross-references: GB:AE005173; NID:g6978918; PIDN:AAF34310.1; GSPDB:GN00141 C.Genetics: A.Gene: F17M19.8 A.Map position: 1</sto>
N:Alternate names: protein F21F14.80 C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000 C;Accession: 747983 R;Choisne, N.; Robert, C.; Brottier, P.; Wincker, P.; Cattolico, L.; Artiguenave, F.; Sasubmitted to the Protein Sequence Database, February 2000	Query Match 26.8%; Score 470.5; DB 2; Length 324; Best Local Similarity 35.1%; Pred. No. 4e-33; Matches 107; Conservative 52; Mismatches 75; Indels 71; Gaps 10;

. Ron	Db 122 VFYGRAPHGOKSDWIMHEYRLDDNIISPEDVTVHEVVSIIGEASQDEGWVVCRIFKKKN 181  Oy 171
A;Status: translated from GB/EMBL/DDBJ A;Status: translated from GB/EMBL/DDBJ A;Residues: Lyge DNA A;Residues: 1.399 cR00> A;Residues: 1.399 cR00> A;Residues: 1.399 cR00> A;Residues: 1.390 cR00> A;Residues: 1.390 cR00> A;Residues: S.;Reunsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujli, C.Y.; M.; Koo, H.; Woffat, K.S.; Cronin, L.A.; Shea, K.; Vanaken, S.E.; Umayam, L.; Tallon, L. euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Shea, K.; Vanaken, S.E.; Umayam, L.; Tallon, L. euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Sealzberg, S.L.; Fraser, C.M.; Venter, J. A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A;Recession: A84907 A;Hele: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A;Recession: A84907 A;Hele: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A;Residues: 1-399 cSTO A;Holecule type: DNA A;Residues: 1-399 cSTO A;Holecule type:	Query Match Best Local Similarity 32.3%; Pred. No. 8.9e-32; Bast Local Similarity 32.3%; Pred. No. 8.9e-32; Matches 120; Conservative 56; Mismatches 91; Indels 104; Gaps 16; Qy 19 LPPGFREHFDDELVCDYLMRRSLHNHRPPLVLIQVDLNKCEPWDIPKANCVGGKD 75 10 VPPGFREHFDDELVCOYLMRRSLHNHRPPLVLIQVDLNKCEPWDIPKANCVGGKD 75 11

10;

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C;Accession: T04050
R;Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Mayer, K. submitted to the Protein Sequence Database, March 1999
A;Reference number: Z15184
A;Accession: T04050
A,Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719
A;Accession: D96683
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-631 <STO>
A;Cross-references: GB:AE005173; NID:g6227016; PIDN:AAF06052.1; GSPDB:GN00141
A;Genetics:
A;Genetics:
A;Map position: 1
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 30-Apr-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         131 PRGRKTDWVMHEFRLQGSHHPPNHSLSSPKEDWVLCRVFHKNTEGVICRDNMGSCFDETA 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                119 PHGSRTDWVMHEYRLE---EQECDSKSGIQDAYALCRVFKKSA--------158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   191 SASLPPLMDPYINFDQEPSSYLSDDHHYIINEHVPCFSNLSQNQTLNSNLTNSVSELKIP 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GKD--WYFYSQRDRKYATGLRTNRATATGYWKATGKDRTILRKGKLVGMRKTLVFYQGRA 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    76 WYFYSQRDRKYATGLRTNRATATGYWKATGKDRTILRKGKLVGMRKTLVFYQGRAPRGRK 135
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Best Local Similarity 34.9%; Pred. No. 2.9e-31;
Matches 112; Conservative 35; Mismatches 97; Indels 77; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14 MVEAKLPPGFRFHPKDDELVCDYLMRRSLHNNHRPPLVLI-QVDLNKCEPWDIPKMACVG 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19 LPPGFRFHPKDDELVCDYLMRRSLHNNHRPPLVLIQVDLNKCEPWDIPKMACVGG---KD 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         159 -----GTKKNKGTTNSEQSTSST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              251 CKNPNPLF------TGGSASATLTGLDSFCSSDQMVLRALLSQLTKIDGSLG-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 25.4%; Score 446.5; DB 2
Best Local Similarity 52.9%; Pred. No. 5.2e-31;
Matches 83; Conservative 27; Mismatches 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          297 PKESQSYGEGSSESLLTDIGI 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      242 PPOSQ-YGTISYPPSKVDIAL 261
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A; Note: F24G24.150
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                                                                                                                                                      Ritheologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Chin, C.W.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Ritle: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719
A;Status: preliminary
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A;Residues: 1.418 <STO>
A;Cross-references: GB:AE005172; NID:g4262176; PIDN:AAD14493.1; GSPDB:GN00141
C;Genetics:
                                 hypothetical protein T2P11.6 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2001
C;Accession: B86395
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15 VEAKLPPGFRFHPKDDELVCDYLMRRSLHNNHRPPL---VLIQVDLNKCEPWDIPKMACV 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     130 APRGRKTDWVMHEFRLQ--GSHHPPN----HSLSSPKEDWVLCRVFHKNTEGVICRDNMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   222 EHVPCFSNLS----QNQTLNSNLTNSVSEL--------KIPCKNPNPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    184 SCFDETASASLPP--LMDPYINFDQEPSSYLSDD------HHYIIN-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26.0%; Score 456; DB 2; Length 418; 34.4%; Pred. No. 1e-31; Live 42; Mismatches 112; Indels
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Matches 128; Conservative
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Gaps

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Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo
ker, M.; Wu, D.; Yu, G.; Eraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719
A;Status: preliminary
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C;Species: Arabidopsis thailand mouse-ear cress)
C;Species: Arabidopsis thailand mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Accession: B95570
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Arceologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, Mature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, A;Authors: Hunter, J.L.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maitl, R.; Marzia Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Accession: B95570
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                                                                                                                                                                                                                                                                                          A; Cross-references: GB: AE005172; NID: 96714280; PIDN: AAF25976.1; GSPDB: GN00141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |: :| || : :| || || 184 -DDCPKITLSSLPD---DTEEEKGPTFHNTQNVTGLDHVLLYMDRTGSNICMPESQTTTQ 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      240 HQDDVLFMQLPSLETP-KSESPV---DQSFLTPSKLDFSPVQEKITERPVCSNWASLDRL 295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     133 GRKTDWVMHEFRLQGSHHPPNHS-----LSSPKEDWVLCRVFHKNTEGVICRDNMGSC 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EAKLPPGFRFHPKDDELVCDYLMRRSLHNNHRPPLVLIOVDLNKCEPWDIPKMACVGG-- 73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             47;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Score 438.5; DB 2; Length 3; Pred. No. 2.8e-30; 61; Mismatches 105; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 436.5; DB 2
Pred. No. 3.5e-30;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25.0%;
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32.9%;
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A; Molecule type: DNA
A; Residues: 1-317 <STO>
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                                                                                                                                                                                                                                 DNA
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A; Map position: 1
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Best Local S
Matches 107
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Nature 408, 816-820, 2000
A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hcpson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A; Tilles, Sequence and analysis of Chromosome 1 of the plant Arabidopsis.
A; Reference number: A86141; MUID:21016719
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Accession: E86452
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Mansen, R.F.; Hughas, B.; Hizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
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                                                                                                                                                                                                                                                     C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Accession: A96570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    76 WYFYSQRDRKYATGLRTNRATATGYWKATGKDRTILRKG----KLVGMRKTLVFYQGRAP 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        73 WYFFSPRDRKYPNGARPNRAATSGYWKATGTDKPVISTGGGGSKKVGVKKALVFYSGKPP 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   133 KGVKSDWIMHEYRL--TDNKPTHICDFGNKKNSLRLDCWVLCRIYKKN------ 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         179 --NSTASRHHHLHHIHLDNDHHRHDMMIDDDRF---RHVPPGLHFPAIFSDNNDPTAIY 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                234 DGGGGGYGGGSYSMNHCFASGSKQEQLFPPVMMMTSLNQDSGIGSSSS------PSKR 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  132 RGRKTDWVMHEFRLQGSHHPPNH----SLSSPKECWVLCRVFHKNTEGVICRDNMGS 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----CFSNLSQNQTL----NSNLTNSVSELKIPCKNPNPL 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16 EAKLPPGFRFHPKDDELVCDYLMRRSLHNNHRPPLVLIQVDLNKCEPWDIPKMACVGGKD 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 86;
                                                                                                                                                                                                                              NAM-like protein, 59502-58357 [imported] - Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                82; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          185 CFDETASASLPPLMDPYINFDQEPSSYLSDDHHYIINEHVP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Score 439; DB 2;
; Pred. No. 2.1e-30;
44; Mismatches 82;
         136 TDWVMHEFRLQGSHHPPNHSLSSPKED-WVLCRVFHK 171
                                           128 TDWIMHEYRLEDADDPQ----ANPSEDGWVVCRVFMK 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25.0%;
32.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 25.0%
Best Local Similarity 32.3%
Matches 101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   258 FTGGSASATLTGL 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               286 FNGGGVGDCSTSM 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-320 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Genetics:
A;Gene: F14G24.15
A;Map position: 1
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Mat	ches	106;	Matches 106; Conservative		51; Mismatches		:06	90; Indels	75; Gaps	Gaps	10;	
Qy	14	MVEAKL	14 MVEAKLPPGFRFHPKDDELVCDYLMRRSLHNNHRPPLVLIQVDLNKCEPWDIPKMACVGG 73	VCDYLMF	RSLHNNHR	PPLVLIO	OVDLN	KCEPWDIP	KMACVC	iG 73		
qq	6	LTQLSL	LTQLSLPPGFRFYPTDEELMVQYLCRKAAGYDFSLQLI-AEIDLYKFDPWVLPNKALFGE 67	MVQYLCF	KAAGYDFS	LOLI-A	EIDLY	KEDPWVLP	NKALFO	E 67		
Qy	74	KDWYFY	74 KDWYFYSQRDRKYATGLRTNRATATGYWKATGKDRTILRKGKLVGMRKTLVFYQGRAPRG 133	NRATATG	YWKATGKD	RTILRK	GKLVG	MRKTLVFY	GRAPI	kG 133		
qq	68		KEWYFFSPRDRKYPNGSRPNRVAGSGYWRATGTDKIISTEGQRYGIKKALVFYIGKAPKG 127	NRVAGSC	YWKATGTD	KIISTE	GORVG	IKKALVFY	GKAPI	(G 127		
Qy	134	RKTDWV	134 RKTDWVMHEFRLQGSHHPPNHSLSSPKEDWVLCRVFHKNTEGVI-CRDNM 182	NHSLSSF	KEDWVLCR	VFHKNT	 	EGVI-	CRD1	M 182		
qq	128	TKTNWI	HHEYRLIEPS	RRNGSTF	LDDWVLCR	IYKKQS	SAQKQ	VYDNGIAN	AREFSI	N 184		
Qy	183	GSCFDE	183 GSCFDETASASLPPLMDPYINFDQEPSSYLSDDHHYIINEHVPCFSNLSQNQTLNSNLT-	INFDQEE	SSYLSDDH	HYIINE	HVPCF	SNLSQNQT	CNSNE	1- 241		
QQ	185	GTSSTT	185 GISSTISSSHFEDVLDSFHQEIDNRNFQ-FSNPNRISSLRPDLTE		H	QEIDNR	NFQ-F	SNPNRISS	LRPDL	E 229		
δy	242	1 1	NSVSELKIPCKNPNPLFT		NSVSELKI	PCKNPN	PLFT -	1	1	GG 261		
qq	230	QKTGFH	230 QKTGFHGLADTSNFDWASFAGNVEHNNSVPELGMSHVVPNLEYNCGYLKTEEEVESSHGF	AGNVEH	NSVPELGM	NGVVHS	LEYNC	GYLKTEEE	VESSH	3F 289		
ΟŊ	262	SASATL	262 SASATLTGLDSFCSSDQM 279	DQM 275								
qq	290	NNSGEL	290 NNSGELAQKGYGVDSFGYSGQV 311	GQV 311								
Searc Job t	h cor ime:	npleted 134 se	Search completed: July 15, 2002, 06:57:27 Job time: 134 sec	02, 06:	57:27							

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GenCore version 4.5
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 protein search, using sw model OM protein July 15, 2002, 06:56:48; Search time 13.42 Seconds Run on:

(without alignments) 934.809 Million cell updates/sec

1757 1 METEEEMKESSISMVEAKLP.......EGSSESLLTDIGIPSTVWNC 324 US-09-889-926-2 Perfect score: Sequence: Title:

Gapop 10.0 , Gapext 0.5 BLOSUM62 Scoring table:

105224 seqs, 38719550 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Maximum Match 100% Listing first 45 summaries Post-processing: Minimum Match 0%

SwissProt\_40:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		æ (				
Result	0400	Query		g	ų,	44.
	a.coze	marcii	reng tu	97	1D	Description
7	106	6.0	1872	-	T2D1_HUMAN	P21675 homo sapien
7	95	5.4	3092	Н	IRA1_YEAST	sacch
e	95		3969	Н	HRX_HUMAN	homo
4	87.5	5.0	314	Н	Y009_HUMAN	Q15390 homo sapien
2	87.5		928	-	PM11_CHLPN	chlam
9	87.5		3866	Н	HRX_MOUSE	
7	86.5		1377	Н	CID_DROME	
80	82	4.8	530	٦	GP2_RAT	
σ	82	4.8	610	П	UVRC_ECOLI	P07028 escherichia
10	84.5	4.8	429	П	NPT1_YEAST	P39683 saccharomyc
11	84.5	4.8	1182	Н	HAIR_MOUSE	
12	84.5	٠	1458	П	PA2R_RABIT	
13	83.5	4.8	337	Н	YDTB_SCHPO	
14	83.5	4.8	591	Н	IF37_ARATH	
15	82.5	4.7	584	٦	ENV_IPMAE	
16	82	4.7	584	Н	YBX1_SCHPO	
17	81.5	4.6	1181	-	HAIR_RAT	
18	81.5	4.6	2222	Н	CCAE_RAT	
19	81	4.6	271	Н	VA04_VARV	P33832 variola vir
20	81	4.6	3125	Н	POLG_PPVNA	
21	80	4.6	368	-	VE2_HPV45	P36794 human papil
22	80	4.6	894	-	FOX2_NEUCR	neuro
23	80	4.6	1142	Н	MGC1_HUMAN	
24	79.5	4.5	454	Н	MUC_HUMAN	homo
25	79.5	4.5	510	Н	YD85_SCHPO	schiz
56	79.5	4.5	765	Н	AMDR_EMENI	-
27	79.5	4.5	696	_	AGLU_SCHPO	Q9c0y4 schizosacch
28	79.5	4.5	1117	7	YN96_YEAST	P53753 saccharomyc
29	79.5	4.5	1210	Н	- 1	P09815 pseudomonas
30	79	4.5	356	Н	- 1	P31363 xenopus lae
31	79	4.5	458	Н	YM51_YEAST	
32	79	4.5	479	П	- 1	Q40082 hordeum vul
33	79	4.5	711	7	RED1_RAT	P51400 rattus norv

	01442/ candida alb P98164 homo sapien							095971 homo sapien	P53863 saccharomyc
KI82_YEAST	CLA4_CANAL LRP2_HUMAN	PCO1_MOUSE	SIR3_YEAST	N153_RAT	MUCB_HUMAN	STA6_MOUSE	CABI_RAT	BY55_HUMAN	YNW7_YEAST
Н,		- 1	+ ~	П	-	П	Н	-	1
726	9/1 4655	468	978	1468	391	837	2182	181	290
2.5	4.4 .5.5	4.5	4.5	4.5	4.4	4.4	4.4	4.4	4.4
79	7 / 6	78.5	78.5	78.5	78	78	78	77.5	77.5
34	3 Q	37	96	40	41	42	43	44	45

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01-MAY-1991 (Rel. 18, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
17ranscription initiation factor TFIID 250 kDa subunit (TAPII-250)
(TAPII250) (TBP-associated factor 250 kDa) (P250) (Cell cycle gene 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBUNIT: TF2D IS COMPOSED OF TBP AND A VARIETY OF TBP-ASSOCIATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY SEQUENCE FROM N.A. MEDIALIZERS SEQUENCE FROM N.A. MEDILIZE-890015.5; PubMed=3108001; Sekiguchi T., Miyata T., Nishimoto T.; Molecular cloning of the cDNA of human X chromosomal gene (CCG1) which complements the temperature-sensitive Gl mutants, tsBN462 and ts13, of the BHK cell line."; EMBO J. 7:1683-1687(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-93196704; PubMed-7680771;
Ruppert S., Wang E.H., Tjian R.;
"Cloning and expression of human TAFII250: a TBP-associated factor implicated in cell-cycle regulation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -1- FUNCTION: MAY PLAY AN ESSENTIAL ROLE IN TFIID ASSEMBLY BY
INTERACTING WITH BOTH TBP AND OTHER TAF, AS WHEL AS SERVING TO
LINK THE CONTROL OF TRANSCRIPTION TO THE CELL CYCLE. ESSENTIAL
FOR PROGRESSION OF THE G1 PHASE OF THE CELL CYCLE. POSSESSES
                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                              TISSUB=Laryngeal carcinoma;
MEDLINE=91246200; PubMed=2038334;
Sekiguchi T., Nohiro Y., Nakamura Y., Hisamoto N., Nishimoto T.;
"The human CCGI gene, essential for progression of the GI phase, encodes a 210 kilodalton nuclear DNA-binding protein.";
Mol. Cell. Biol. 11:3317-3325(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "The p250 subunit of native TATA box-binding factor TFIID is the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hisatake K., Hasegawa S., Takada R., Nakatani Y., Horikoshi M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SUBCELLULAR LOCATION: Nuclear.
-!- PTM: PHOSPHORYLATED BY CASEIN KINASE II IN VITRO.
-!- SIMILARITY: CONTAINS 2 BROMODOMAINS.
                                                                                           PRT; 1872 AA.
ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A., AND CHARACTERIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cell-cycle regulatory protein CCG1.";
Nature 362:179-181(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHARACTERIZATION.
MEDLINE=93196705; Pubmed=8450888;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 362:175-179(1993).
                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA-BINDING ACTIVITY
                                                                                                                                                                                                                                       TAFZA OR CCG1 OR BAZR.
                                                                                                                                                                                                                                                                    (Human)
                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Roeder R.G.;
                                                                                   T2D1_HUMAN
P21675;
                                                                                                                                                                                                                                 protein)
                                                       RESULT 1
T2D1_HUMAN
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us-09-889-926-2.rsp

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1330 IESADEVRRKSLVLKFPKQQLPPKKRRRVGTTVH------CDYLNRPHKSIHRRRTDPM 1382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1383 VTLSSILESIINDMRDLPNTYPFHTPVNAKV-VKDYYKIITRPMDLQT-LREN----- 1433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -------VRKRL--YPSR------BEFREHLELIVKNSATYNGP 1462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1463 KHSLTQISQSMLDLCDEKLKEKEDKLAR-----LEKAINPLLD---DDDQVAFSF 1509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1570 DDVNLILANSVKYNGPESQYTKTAQEIVNVCYQTLTEYDEHLTQLEKDICTAKEAALEE- 1628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             101 WKATGKDRTILRKGKLVGMRKTLVFYQGRAPRGRKTDWWMHEFR-----LQGSHHPP 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            regulation; Phosphorylation.
7 165 PRO-RICH.
15 1273 HMG BOX (POTENTIAL).
1 1358 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51 VLIQV-----DLNKCEPWDIPKMACVGGKDWYFYSQRDRKYATGLRTNRATATGY 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 METEEEMKESS--ISMVEAKLPP-----GFRFHPKDDJELVCDYLMR--RSLHNNHRPPL 50
SIMILARITY: CONTAINS 1 HMG BOX. SIMILARITY: TO DROSOPHILA TAFII-230. SOME TO S.POMBE TAFII-111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---NSVSELKIPCKNPNPLFTGGSAS-----ATLTGLD-----SFCSSDQMVLRAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        153 NHSLSSPKEDWV-LCRVFHKNTEGVICRDNMGSCFDEJTASASLPPLMDPYINFDQEPSSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----HHYIINEHVPCFSNLSQN ---QTLNSNLT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 6.0%; Score 106; DB 1; Length 1872; Best Local Similarity 19.9%; Pred. No. 0.37; Matches 79; Conservative 51; Mismatches 125; Indels 142;
                                                                                                                                                                                                                                                                                                                                                                            PRINTS, PRODSO3; BROMODOMAIN.
SMART; SM00297; BROMO; 2.
PROSITE; PS0063; BROMODOMAIN_1; 2.
PROSITE; PS50014; BROMODOMAIN_2; 2.
Bromodomain; Nuclear protein; DNA-binding; Cell cycle; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ASP/GLU-RICH (ACIDIC TAIL). MW; 93BE3D181A72ABEB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1629 -AELESLDPMTPGPYTPQPPDLYDTNTSLSMSRDASV 1664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     285 LSQLTKID----GSLGPKESQSYGEGSSESLLTDIGI 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BROMODOMAIN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BROMODOMAIN 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                              EMBL; D90359; BAA14374.1; -.
EMBL; X07024; CAA30073.1; ALT_SEQ.
                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001487; Bromodomain.
                                       AND TO S.CEREVISIAE TAF145.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IRA1_YEAST STANDARD;
P18963;
01-NOV-1990 (Rel. 16, Created)
                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00439; bromodomain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              212676
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1590
1872
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1397 146
1520 159
1627 187
                                                                                                                                                                                                                                                                                                       TRANSFAC; T02206; -.
                                                                                                                                                                                                                                                                 PIR; S03005; S03005.
PIR; A40262; A40262.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Transcription
DOMAIN 15
                                                                                                                                                                                                                                                                                                                          MIM; 313650;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA_BIND
DOMAIN
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between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                           MEDILINE 59274325; PubMed=7754712; Zagulski M., Becam A.-M., Grzybowska E., Lacroute F., Migdalski A., Slonimski M., Becam A.-M., Grzybowska E., Lacroute F., Migdalski A., Slonimski P.P., Sokolowska B., Herbert C.J.; "The sequence of 1.5 kb from the right arm of chromosome II predicts a new N-terminal sequence for the IRAl protein and reveals two new genes, one of which is a DEAD-box helicase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "The sequence of 29.7 kb from the right arm of chromosome II reveals 13 complete open reading frames, of which ten correspond to new
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Becam A.-M., Cullin C., Grzybowska E., Lacroute F., Nasr F.,
Ozier-Kalogeropoulos O., Palucha A., Slonimski P.P., Zagulski M.,
                                                                               Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                              Tanaka K., Matsumoto K., Toh-E A.; "IRA1, an inhibitory regulator of the RAS-cyclic AMP pathway in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTPASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         I- FUNCTION: INHIBITORY REGULATOR OF THE RAS-CYCLIC AMP
PATHWAY IN SACCHAROMYCES CEREVISIAE. STIMULATES THE G
ACTIVITY OF RAS PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 > G (IN REF. 2).
291339AE5BD26E08 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PHOSPHORYLATION (BY CAPK)
                                                                Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Sacch
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
01-0CT-1994 (Rel. 30, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Inhibitory regulator protein IRAl:
IRAL OR PPD1 OR GLC1 OR YBR140C OR YBR1016.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: CONTAINS 1 RAS-GAP DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00509; RAS_GTPASE_ACTIV_1; 1.
PROSITE; PS50018; RAS_GTPASE_ACTIV_2; 1.
GTPase activation; Phosphorylation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=94378717; PubMed=8091856;
                                                                                                                                                                                                                                                                                                                                                                                            Mol. Cell. Biol. 9:757-768(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 2768-3092 FROM N.A.
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EMBL, X75891; CAA53489.1; -.
EMBL, Z36009; CAA85098.1; -.
EMBL, X78937; CAA55537.1; -.
PIR, S46009; S46009.
SGD, S0000344; IRA1.
InterPro; IPR001936; RasGAP.
                                                                                                                                                SEQUENCE OF 1-2767 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00616; RasGAP; 1.
SMART; SM00323; RasGAP; 1
                                                                                                                                                                                                                                                                              Yeast 10:1227-1234(1994).
                                                                                                                                                                                                                                                                                                                                                                                Saccharomyces cerevisiae
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3092 AA;
                                                                                                                 NCBI_TaxID=4932;
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350974 MW;

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MEDLINE-93390935; PubMed=8378076;
Yamamoto K., Seto M., Komatsu H., Iida S., Akao Y., Kojima S.,
Kodera Y., Nakazawa S., Ariyoshi Y., Takahashi T., Ueda R.;
"Two distinct portions of LTG19/ENL at 19913 are involved in t(11;19)
                                                                                                                                                                                             :| ||: | :| | :| | :| | :| | | :| | | :| | | :| | | :| | | | :| | | | :| | | | :| | | | :| | | | :| | | | :| | | | :| | | | :| | | | :| | | | :| | | | :| | | | :| | | | :| | | | :| | | :| | | | :| | | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | 
                                                                                                                                                                                                                                                                                       81 QRDRKYATGLRTNRATATGYWKATGKDRTILRKGKLVGMRKTLVFYQGRAPRGRKTDWV- 139
                                                                                                                                                                                                                                                                                                                                                          264 YLTDKNLLAYLDILQHLSSYMK-----RTIFHSLLLYYASKAFLFWIMARPK----EYVK 314
                                                                                                                                                                                                                                                                                                                                                                                                                                140 MHEFRLQGSHHPPNHSLSSPKEDWVLCRVFHKNTEGVICRDNMGS-CFDETASASLPPLM 198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           352 FDDVYSTF--SVSSLITNVNNDHHYHLHH-----SSSSSKTTNTNSPNSISKTSIKQSS 403
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   315 IYNNLISSDYNSPSSS------SDVGGSNNSDKTSISQLVSLL 351
                                                                                                                                         31 ELVCDYLMRRSLHNNHRPPLVLIQVDLNKCEPWDI------PKMACVGGKDWYFYS 80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=96290553; PubMed=8703835;
Nilson I., Loechner K., Siegler G., Greil J., Beck J.D., Fey G.H.,
Marschalek R.;
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
   5.4%; Score 95; DB 1; Length 3092; 21.7%; Pred. No. 7.2; ative 46; Mismatches 121; Indels
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Tkachuk D.C., Kohler S., Cleary M.L.,
Involvement of a homolog of Drosophila trithorax by 11q23
chromosomal translocations in acute leukemias.";
Cell 71:691-700(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HRX_HUMAN STANDARD; PRT; 3969 AA. 003164; Q14845; Q16364; Q13743; Q13744; Q9UMA3; Q10-OCT-1993 (Rel. 27, Created) 01-NOV-1995 (Rel. 32, Last sequence update) 01-MAR-2002 (Rel. 41, Last annotation update) Zinc finger protein HRX (ALL-1) (Trithorax-like protein). MLL OR HRX OR ALL1 OR TRX1 OR HTRX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 1317-2328 FROM N.A.
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                                                                              Conservative
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                                     Similarity
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SEQUENCE FROM N.A.
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Query Match
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                                 Best Local
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T (3:11) (P21:q23).";

RL Blood 9:1066-1066(2000).

C -: FUNCTION: POSSIBLA FACTS AS A TRANSCRIPTIONAL REGULATORY FACTOR.

C -: SUBGELLUAR LOCATION: Nuclear.

C -: SUBGELLUAR LOCATION: Nuclear.

C -: TISSUE SPECIFICITY: HEART, LUNG, BRAIN AND T AND B LYMPHOCYTES.

C -: DISEASE: INVOLVED IN ACUTE LEUKEMIAS BY CHROMOSOMAL TRANSLOCATIONS

CC -: DISEASE: INVOLVED MA ACUTE LEUKEMIAS BY CHROMOSOMAL TRANSLOCATIONS

CC T(11:19) (Q23:P13.3) THAT INVOLVES MLL AND MLLTZ/AR4; T(9:11) (P22:Q23)

THAT INVOLVES MLL AND MLLT3/AR9; T(6:11) (Q27:Q23) THAT INVOLVES MLL AND MLLTD/ARX1;

CC T(10:11) (P12:Q23) THAT INVOLVES MLL AND MLLTO/AFX1;

CC T(11:11) (Q21:Q23) THAT INVOLVES MLL AND AF10; T(11:19) (Q23:P13:3)

CC T(11:11) (Q21:Q23) THAT INVOLVES MLL AND AF10;

CC -: SIMILARITY: CONTAINS 1 BROMODOMIN.

CC -: SIMILARITY: CONTAINS 1 BROMODOMIN.

CC -: SIMILARITY: CONTAINS 3 PHD-TYPE ZINC FINGERS.

CC -: SIMILARITY: CONTAINS 1 CXXC-TYPE ZINC FINGERS.
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                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 1212-1603 FROM N.A.
MEDLINE=95315013; PubMed=7794749;
Marschalek R., Greil J., Lochner K., Nilson I., Siegler G.,
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"A method for identifying genes within yeast artificial chromosomes:
application to isolation of MLL fusion cDNAs from acute leukaemia
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                                                                                                                                                                                                                                                                                               Mbangkollo D., Burnett R., McCabe N., Thirman M., Gill H., Yu H., Rowley J.D., Diaz M.O.;
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translocations in acute leukaemias.";
Nat. Genet. 2:113-118(1992).
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                                                                SEQUENCE OF 1251-1538 FROM N.A.
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the European Bioinformatics Institute. There are no restrictions on
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EMBL, S6643; AAG2845.1; -.
EMBL, R5231998; AAG26332.2; ALT_TERM.
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Alternative splicing.

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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MEDLINE=96051387; PubMed=7584026;
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MEDLINE=99081766; PubMed=9864239;
Knudsen K., Madsen A.S., Mygind P., Christiansen G., Birkelund S.;
"Identification of two novel genes encoding 97- to 99-kilodalton outer membrane proteins of Chlamydia pneumoniae.";
Infect. Immun. 67:375-383(1999).
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GYANDARD; PRT; 928 AA.
086164; 09K299;
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
Probable outer membrane protein pmp11 precursor (Polymorphic membrane protein 1)
Probable outer membrane protein 4).
PRP11 OR OMP4 OR CPN0449 OR CP0312.
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                                                                                                                                                                                                                                                                                                                                             Length 314;
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Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila.
NCBL_TaxID=83558;
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MEDLINE=20007584; PubMed=10539856;
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RM11_CHLPN
ID PM11_COLD
AC 08616_CI
DT 16-OCT
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F., White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S., Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R., Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L., Eisen J., Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  106 KDRTILRKGKLV-----GMRKTLVFYQGRAPRGRKTDWV-----MHE----- 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      :| | : | | : | | : | | | 112 QPQNYLRIGRAKFSESAIEKFPREIPLALDVQVSFSH--SDNRMETHYTSLPE----- 762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              50 LVLIQVDLNKCEPWDIPKMACVGGKD----WYFYSQRDRKYATGLRINRATATGYWKATG 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       532 LLKITVDADVDTNVDISSLIPVPAEDPNSEYGFQGQWNVNWTTDTATNTKEATATWTKTG 591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              182 -----MGSC-FDETASASLP---PL-MDPYINFDQEPSSYLSDDHHYIINEHVPCFSN 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 230 LSQNQTLNSNLTNSVS-ELKIPCKNPNPLFTGGSASATLTGLDSFCSSDQMVLRALLSQL 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          592 FVPSPERKSALVCNTLWGVFTDIRSLQQLVEIGATGMEHKQGFWVSSMTNFLHKTGDENR 651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----KTFIPQM 798
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                                                                                                                                                                                                                                                          Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K., Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.; "Comparison of whole genome sequences of Chlamydia pneumoniae J138 from Japan and CWL029 from USA."; Nucleic Acids Res. 28:2311-2314(2000).

-:- SUBCELLULAR LOCATION: CELL WALL SURFACE (ELEMENTARY BODIES)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROBABLE OUTER MEMBRANE PROTEIN PMP11.
788BCDD62C911402 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SIMILARITY: BELONGS TO THE PMP OUTER MEMBRANE PROTEIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66
                                                                                                            "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Outer membrane; Signal; Multigene family; Complete proteome.
SIGNAL 1 24 POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     143 --FRLQGSHHPPNHSLSSPKED---WVLCRVFHKNTEGVICRDN--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 5.0%; Score 87.5; DB 1;
Best Local Similarity 20.4%; Pred. No. 6.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    289 TKIDGSLGPK----ESQSYGEGSSESLLTDIGIP 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
                                                                                                                                                       Nucleic Acids Res. 28:1397-1406(2000).
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EMBL; AJ133034; CAB37072.1; -.
EMBL; AE001628; AAD18593.1; -.
EMBL; AE002192; AAF38159.1; ALT_INIT.
EMBL; AP002246; BAA98658.1; -.
PHCI-2DPAGE; O86164; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            763 -SEGSWSNECIAGGIGLDLPFVLSNPHPLF
                                                                                                                                                                                                                      STRAIN-J138;
MEDLINE-20330349; PubMed-10871362;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25 928 P
928 AA; 98903 MW;
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InterPro; IPR003357; OMP.
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Pfam; PF02385; OMP; 1.
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                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                  pneumoniae
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799 -KVEMVYVSQNSFFESSSDGRGFSIGRLLNLSIP 831

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SUBCELLULAR LOCATION:
SUBCELLULAR LOCATION:
2 ISOPORMS: 1 (SHOWN HERE) AND 2; ARE
PRODUCED BY ALTERNATIVE SPLICING.
SIMILARITY: BELONGS TO THE TRANSCRIPTION FACTOR TRITHORAX FAMILY.
SIMILARITY: CONTAINS 1 BROMODOMAIN.
SIMILARITY: CONTAINS 1 SET DOMAIN.
SIMILARITY: CONTAINS 3 PHD-TYPE ZINC
SIMILARITY: CONTAINS 1 STD DOMAIN.
SIMILARITY: CONTAINS 1 STD CONTAINS SIMILARITY: CONTAINS 1 STD CONTAINS SIMILARITY: CONTAINS 1 STD CONTAINS SIMILARITY: CONTAINS 1 CXXC-TYPE ZINC FINGERS.
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-!- FONCTION: POSSIBLY ACTS AS A TRANSCRIPTIONAL REGULATORY FACTOR. MAY REGULATE GENES INVOLVED IN SKELETAL FORMATION DURING EMBRYONIC DEVELOPMENT.
                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi; Muridae, Murinae; Mus
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PROSITE; PS50280; SF7. 1.
DNA-binding; Nuclear protein; Zinc-finger; Metal-binding;
Transcription regulation; Alternative splicing; Polymorphism.
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A.T HOOK (BY SIMILARITY).
A.T HOOK (BY SIMILARITY).
                                                                                                                                                                                                                       01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-MR-2002 (Rel. 41, Last annotation update)
MLL of tinger protein HRX (ALL-1) (Fragment).
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                                                                                                                                                      STANDARD;
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115
199
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                                                                                                                                                      HRX_MOUSE
P55200;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                86 YATGLRINRATATGYWKATGKDRIILRKGKLVGMRKTLVFYQGRAPRGRKTDWVMHEFRL 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        198 MDP-YINFDQEP-----SSYLSDDHHYIINEHVPCFSNLSQNQTLNSNLTNSVSELKI 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                250 PCKNPNPLFTGGSASATL-----TGLDSFCSSDQMVLRALLSQLTKIDGSLGPKESQ 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    146 QGSHHPPNHSLSSPKEDWVLCRVF-----HKNTEGVICRDNMGSCFDETASASLPPL 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                             43; Mismatches 140; Indels 77; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                          38 MRRSLHNNHRPPLVLIQV------BLNKCEPWDIPKMACVGGKDWYFYSQRDRK 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Berry A.J., Ajioka J.W., Kreitman M.; "Lack of polymorphism on the Drosophila fourth chromosome resulting from selection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Orenic T.V., Slusarski D.C., Kroll K.L., Holmgren R.A.; "Cloning and characterization of the segment polarity gene cubitus interruptus Dominant of Drosophila."; Genes Dev. 4:1053-1067(1990).
                                                                                                                                                                                                                                                                                                                                 Length 3866;
                                                                                                                                                                                                                                                                  420976 MW; ADFC55E14E806F1D CRC64;
PHD-TYPE 1.
PHD-TYPE 2.
PHD-TYPE 3.
BROMODOMAIN (DIVERGENT).
                                                                                                                                                                                                                           MISSING (IN ISOFORM 2).
                                                                                                                                                                                                                                                                                                                                      DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT; 1377 AA.
                                                                                                                                                                                                                                                                                                                                      1 5.0%; Score 87.5; I Similarity 19.5%; Pred. No. 46;
                                                                                                                                                                              POLY-GLU.
POLY-GLU.
                                                                                                             POLY-GLY
                                                                                                                                                         POLY-PRO
                                                                                                                                  PRO-RICH
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                                                                                                                                                                                                                                                    STRAIN=OREGON-R;
MEDLINE=92146935; PubMed=1686006;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2167 QRTVGGSKTSHLDGSSPSEVKRC 2189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=OREGON-R;
MEDLINE=90346286; PubMed=2166702;
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                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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469
1238
3536
3697
1381
1432
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3846
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                                                                                                                                                                                                                                                                       3866 AA;
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NCBI_TaxID=7227;
                                         1465
1605
3737
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3693
1503
1497
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P19538;
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Best Local 8
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[1]
SEQUENCE FROM N.A.
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CARBOHYD
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Matches
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                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
Genetics 129:1111-1117(1991).

-!- FUNCTION: INVOLVED IN SEGMENT POLARITY. IS REQUIRED FOR THE NORMAL DEVELOPMENT OF THE POSTERIOR HALF OF EACH EMBRYONIC SEGMENT.
-!- SUBCELLULAR LOCATION: Nuclear.
-!- DEVELOPMENTAL STRAGE: EXPRESSED UNIFORMLY THROUGHOUT THE BLASTODERM STAGE AND GASTRULATION AND DOES NOT RESOLVE INTO SEGMENTALLY REPEATING STRIPES UNTIL THE END OF THE SHORT PHASE OF GERM-BAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MOV-1990 (Rel. 16, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Pancreatic secretory granule membrane major glycoprotein GP2 precursor (Pancreatic zymogen granule membrane protein GP-2) (Glycoprotein 80)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1057 SIKADWAMTSDQHPNE-----RINL-----BEVEELILPDEMLQYLNLVKDDTNHLEKEH- 1106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1107 ----QAVPVGSNVSETIASNHYREQSNIYYTNKQILTPPSNVDIQPNTTFTVQDKFAMTA 1162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            158 SPKEDWVLCRVFHKNTEGVICRDNMGSCFDETASASLPPLMDPYINFDQEPSSYLSDDHH 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           218 YIINEHVPCFSNLSQNQTLN----SNLTNSVSELKIPCKN----PNPLFTGGSASATLT 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31; Gaps
                                                                                                                                                                                                                                                                                                        PROUDSU, SINCEINGE. SERVERS; PROUDSU, SHART; SMOO35; ZINCEINGE. C2H2_1; 4. SMART; SMOO355; ZINC_FINGER_C2H2_2; 4. PROSITE; PSOO157; ZINC_FINGER_C2H2_2; 4. Developmental protein; Segmentation polarity protein; Zinc-finger; Metal-binding; DNA-binding; Repeat; Nuclear protein. 603 ZINC FINGERS. *76 * C2H2-TYPE.
                                                                                                 SIMILARITY: TO THE GLI-RELATED GROUP OF C2H2-TYPE ZINC-FINGERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4.9%; Score 86.5; DB 1; Length 1377; 25.6%; Pred. No. 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1163 VGGSFSQRE-----LSTLA-VPNEHGHAKCESFHQSQKYMNTDIG 1202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           269 GLDSFCSSDQMVLRALLSQLTKIDGSLGPKESQSYGEGSSESLLTDIG 316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        150881 MW; 85189314D5E7B3B7 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               530 AA
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C2H2-TYPE.
                                                                                                                                                                                                                                                                                                InterPro; IPR000822; Znf-C2H2.
Pfam; PF00096; zf-C2H2; 5.
PRINTS; PR00048; ZINCFINGER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1990 (Rel. 16, Created)
                                                                                                                                                                                                                                   EMBL; X54360; CAA38244.1; -.
                                                                                                                                                                                                                                                                                  FlyBase; FBgn0004859; ci.
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                                                                                                                                                                                                                                               PIR; A35817; A35817.
PIR; S12769; S12769.
                                                                                                                                                                                                                                                                                                                                                                                                                                  517 54
547 57
578 60
1377 AA;
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                                                                                                              PROTEINS.
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Local Si.
43;
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ZN_FING
SEQUENCE
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P19218;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92; Gaps
                                                                                                                                                                                                                                                                                                                J. Biol. Chem. 266:4257-4263(1991).
-1- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR, THEN CLEAVED TO PRODUCE A SOLUBLE FORM WHICH IS SECRETED IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PANCREATIC SECRETORY GRANULE MEMBRANE
                                                                           Nucleotide sequence encoding the major glycoprotein (GP2) of rat
                                                                                                                                                                   SEQUENCE FROM N.A., AND SEQUENCE OF 293-303 AND 477-495.
MEDLINE-91154223; PubMed-1999417;
Hoops T.C., Rindler M.J.;
"Isolation of the cDNA encoding glycoprotein-2 (GP-2), the major
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (POTENTIAL). (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                         PANCREATIC JUICE.
-!- TISSUE SPECIFICITY: PANCREATIC SECRETORY (ZYMOGEN) GRANULE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          45; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -> H (IN REF. 2).
-> V (IN REF. 2).
97A3CDD019BC7DFF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Glycoprotein; Pancreas; Membrane; Signal; GPI-anchor;
EGF-like domain.
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BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC...) (
                                                                                               pancreatic secretory (zymogen) granule membranes."; Nucleic Acids Res. 18:5900-5900(1990),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MAJOR GLYCOPROTEIN GP2
                                                                                                                                                                                                                                                                     zymogen granule membrane protein. Homology to
uromodulin/Tamm-Horsfall protein.";
                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
-!- SIMILARITY: CONTAINS 1 2P DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4.8%; Score 85; DB 19.0%; Pred. No. 5.2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000561; EGF-1ike.
InterPro; IPR001507; zona_pellucida.
Pfam: PF00100; zona_pellucida; 1.
PRINTS; PR00023; ZPELLUCIDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PRUUULL, ...
SNART; SM00241; ZP; 1.
PROSITE; PS00022; EGF_1; FALSE_NEG.
PROSITE; PS01186; EGF_2; FALSE_NEG.
---- DS00682; ZP_DOMAIN; 1.
STRAIN-WISTAR; TISSUE-Pancreas; MEDLINE=91016950; PubMed=2216794;
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Μ.
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EMBL, M89716; AAA41268.1; -.
PIR, S11503; S11503.
PIR, A38690; A38690.
                                               Jukuoka S.-I., Scheele G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58708
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MEDLINE-97251358; PubMed-9097040;
Itoh T. Alba H., Baba T., Fuljta K., Hayashi K., Inada T., Isono K.,
Itoh T., Alba H., Baba T., Fuljta K., Hayashi K., Inada T., Isono K.,
Kasai H., Kimura S., Kitakawa M., Kitagawa M., Makino K., Miki T.,
Mizobuchi K., Mori H., Mori T., Motomura K., Nakade S., Nakamura Y.,
Nashhaoto H., Nishio Y., Oshima T., Saito N., Sampei G., Seki Y.,
Yamamoto Y., Horluchi T.; Takeda J., Takemoto K., Wada C.,
Yamamoto Y., Horluchi T.;
A 460-kb DNA sequence of the Escherichia coli K-12 genome
corresponding to the 40.1-50.0 min region on the linkage map.";
-----PYIN-----FDQEPSSYLSDD- 215
                                    211 SDTLSLQPLLDCGANEIKVKLDKCLLGGLGFKEDIITYLNDRNCRGTMKDEPNNWVSTTS 270
                                                                          -----HHYIINEHVPCFSNLSQNQTLNSNLTNS 243
                                                                                                  271 PVVANDCGNILENNGTQAIXRNTLSLATDFIIRDFLVNVNFQCAYPLDMNVSLQTALQPI 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Moolenaar G.F., van Sluis C.A., Backendorf C., van de Putte P.; "Regulation of the Escherichia coli excision repair gene uvrC. Overlap between the uvrC structural gene and the region coding for a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-K12 / MG1655;
MEDLINE-97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Fode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-86176730; PubMed-3515318; Sharma S., Stark T.F., Beattie W.G., Moses R.E.; "Multiple control elements for the uvrC gene unit of Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE-84247323; Pubwed-6330676;
Sancar A., Rupp W.D.;
"Sequences of the E. coli uvrc gene and protein.";
Nucleic Acids Res. 12:4593-4608(1984).
                                                                                                                                                                                                                                                                                         UVRC_ECOLI STANDARD; PRT; 610 AA.. p07028; P76311; Created) 10-ARH-1988 (Rel. 32, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Excinuclease ABC subunit C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic Acids Res. 15:4273-4289(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic Acids Res. 14:2301-2318(1986).
                                                                                                                                                        244 VSELKIPCKNPNPLFTGGSASATLT 268
                                                                                                                                                                                          331 VSSLNVD-----VGGAGEFTVT 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 1-28 FROM N.A. MEDLINE-87231005; PubMed-3295776;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 604-610 FROM N.A. MEDLINE-8$111778; Pubmed-3003065;
  189 TASASLPPLMD------
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                                                                                                                                                                                                                                                                                                                                                                                                                           Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=562;
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238 RVTEKQFVSNTGDDLDVIGVAFDAGMACVHVLFIROGKVLGSRS----YFPKVPGGTKLS 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       138 WVMH----EFRLQGSHHPPNHSLSSPKEDWVLCRVFHKNTEGVICRD-NMGSCFDETASA 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  294 EVVETFVGQFYLQGSQ-----DKTLLPGEILLDFNLS---DKTLLA 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              193 -SLPPLMDPYINFDQEPSSYLSDDHHYI----INEHVPCFSNLSQNQTLNSNLTNSVSEL 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        331 DSLSELAGRKINVQTKPR---GDRARYLKLARTNAATALTSKLSOOSTVHORLTALASVL 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Excision nuclease; DNA repair; Complete proteome. 1.1 291 K -> E (IN REF. 3 AND 4). AA; 68187 \text{ MW}; C347C4606FACB926 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4.8%; Score 85; DB 1; Length 610; 25.7%; Pred. No. 6.3; ive 17; Mismatches 63; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        429 AA.
                                                                                                                                                                                                                                                                                                                           EMEL; AECOCCA4; AAC74980.1; ALT_INIT.
EMEL; D90832; BAA15733.1;
EMEL; M12299; AAA88753.1; -.
PIR; A22863; BVECUC.
PIR; A224644; C244944.
ECOZDBAAE; 1065.0; GTH EDITION.
                                                                                                                                                                                                                                                                                                   EMBL; X03691; CAA27329.1; ALT_INIT.
EMBL; M24615; AAA24756.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000445; HHH.
InterPro; IPR001943; HHH.1.
InterPro; IPR001162; UVR.
InterPro; IPR001162; UVR.
InterPro; IPR000305; UVR.
Pfam; PF01541; Exci_endo_N; 1.
Pfam; PF01633; HHH; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NOTI_YEAST STANDARD; 1
P39683; Q08626;
01-FEB-1995 (Rel. 31, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  68187 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF02151; UVR; 1.
ProDom; PD005870; UVRC_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART; SM00465; GIYC; 1.
SMART; SM00278; HhH1; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   610 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOS response; Ex
CONFLICT 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        248 KIP 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  388 KLP 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 10
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       qq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66 TEEE-----IEYLKQEIPYLPSAXIKYISSSNYKLHPEEQISFTSEEIEGKPTHYKLK-- 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                89 GLRTNRATAT ----- GYWKAT -- GKDRTILRKGKLVGMRKTLVFYQ-GRAPRGRKT-DW 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               139 VMHEFRLQGSHHPPNHSLSSPKEDWVLCRVFHKNTEGVICRDNMGSCFDETASASLPPLM 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels 123; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 TEEEMKESSISMVEAKLP------PGFRFHPKDD-ELVCDYLMRRSLHNNHRPP 49
                                                                                                                                                                                                                                                                                                                                                                           Lalo D., Carles C., Sentenac A., Thuriaux P.; "Interactions between three common subunits of yeast RNA polymerases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YEIPLLS -> MRSLTV (IN REF. 1).
FKFVDIDWDYENQLEQ -> LIVTSTGLRNHRQ (IN
                                                                                                                                                                                                                                                                                                                                                                                                                           Proc. Natl. Acad. Sci. U.S.A. 90:5524-5528(1993).
-!- CATALYTIC ACTIVITY: Nicotinate D-ribonclectide + diphosphate nicotinate + 5-phospho-alpha-D-ribose 1-diphosphate.
-!- PATHWAY: FIRST STEP IN PREISS-HANDLER PATHWAY LEADING TO THE
                                                                                   Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 429;
01-%0V-1997 (Rel. 35, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Probable nicotinate phosphoribosyltransferase (EC 2.4.2.11)
                                                                                                                                                                                                                                                                        Hughes B., Pohl T.M.;
Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                     Lalo D., Doira C., Thuriaux P.; Submitted (JAN-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50 LVLIQVDLNKCEPWDIPKMACVGGK-----DWYF---YSQRDRKYAT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E -> EL (IN REF. 1).
F3F7941476C3398B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REF. 1).
SEF -> RIH (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4.8%; Score 84.5; DB 1;
18.4%; Pred. No. 4.3;
ive 56; Mismatches 140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: BELONGS TO THE NAPRTASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                          MEDLINE=93296170; PubMed=8516295;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Glycosyltransferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      49018 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; Z75117; CAA99424.1; -. EMBL; L11274; AAB59317.1; -. PIR; S48884; S48884.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; Z36878; CAA85352.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18.4%;
                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 1-43 FROM N.A. STRAIN=FL100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SYNTHESIS OF NAD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      243
429 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S0005735; NPT1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
                                                                                                                                                                                                                                                         N.A.
                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                      NCBI_TaxID=4932;
                                                                   NPT1 OR YOR209C.
                                                                                                                                                                                                                                                       SEQUENCE FROM
                                                                                                                                                                                         STRAIN-FL100;
                                                                                                                                                                                                                                                                                                                                                                                                               I and III.";
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                                                    (NAPRTase)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INCLUDING STRUCTURAL ABNORWALITIES OF EPITHELIAL CELLS IN THE HAIR FOLLICLES, HAIR LOSS TOWARDS THE END OF THE FIRST HAIR GROWTH CYCLES, AND THE FAILURE OF SUBSEQUENT HAIR GROWTH CYCLES. OLDER MICE CARRYING AN HR WUTATION HAVE BEEN REPORTED TO POSSESS ALFERED RATIOS OF T-CELL-DEPENDENT B-CELL RESPONSES. MICE HOMOZYGOUS FOR HR MUTATION ARE UNIQUELY SENSITIVE TO UV AND CHEMICALLY INDUCED
  237
                        ----SNLTNSVSELKIPCKNPNPLFTGGSASATLTGLDSFCSSDQMVLRALLSQLTK 290
                                                                                                                -----NIVIKLLE 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Proc. Natl. Acad. Sci. U.S.A. 91:7717-7721(1994).
-!- FUNCTION: MAY ACT AS A TRANSCRIPTION FACTOR THAT COULD ACT ON TO REGULATE ONE OF THE PHASES OF HAIR GROWTH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF02373; jmjC; 1.
Zinc-finger; DNA-binding; Nuclear protein; Transcription regulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISEASE: HR MUTATION PRODUCES A NUMBER OF PLEIOTROPIC EFFECTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-BALB/C; TISSUE-Skin;
MEDLINE-94329587; PubMed-8052649;
Cachon-Gonzalez M.B., Fenner S., Coffin J.M., Moran C., Best S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -:- SUBCELLULAR LOCATION: Nuclear.
-:- TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN BRAIN, HAIR
FOLLICLES AND INTERFOLLICULAR EPIDERMIS. NO EXPRESSION IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Stoye J.P.;
"Structure and expression of the hairless gene of mice.";
"Astructure and expression of the hairless gene of mice.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10 POLY-GLY.
127182 MW; EFBB0EE62AE81B40 CRC64;
199 DPYINFDQ---EPSSYLSD-DHHYIINEHVPCFSN-LSQNQTLN--
                                                                                                                                                                                                                                                                                                                                 01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                              PRT; 1182 AA
                                                                                                                348 LATFGIGTNFTNDFRKKSEPQVKSEPL-----
                                                                                                                                                         291 IDGSLGPKESQSYGEGSSESLLTDIGIPSTV 321
                                                                                                                                                                                              383 VNGNHAIKISDNLGK-----NMGDPATV 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; Z32675; CAA83587.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Interpro, IPR003347; JmjC.
                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              535 54
1182 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                      musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                          16-OCT-2001 (Rel. Hairless protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MGD; MGI:96223;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SKIN TUMORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Metal-binding.
                                                                                                                                                                                                                                                                                            HAIR_MOUSE
Q61645;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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DOMAIN
                                                                                                                                                                                                                                                       RESULT 11
                                                                           238
                                                                                                                Dp
                                  g
                                                                           δ
                                                                                                                                                         δλ
                                                                                                                                                                                                                                                                                              Qγ
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Gaps

89;

Indels

16; Mismatches

59; Conservative

Best Local Similarity

Matches

Query Match

4.8%; Score 84.5; DB 1; Length 1182; 23.0%; Pred. No. 17;

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                                61 LPPGFLOGPKDTLSLVEGEGPRNGERKGSWLGGKEGLRWKEAMLAHPLAFCGPACPPRYG 120
                                                                                                                                       264
                                                                                                                                                                                                                                           198 AFGLGSKGFYHKDPNILRPAKEPLAE-SGMLGLAPGGHLQQACESEGPSLHQRDGETGAG 256
111 LRKGKLVGMRKTLVFYQGRAPRG--RKTDW------VMHEFRLQGSHHP---- 151
                                                                                                     167
                                                                                                                                                                        ------PNPWVYSGSQPKVPS 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             phosphoilpases A2.";
J. BA10. Chem. 269:1575-1578(1994).
-1- FUNCTION: MAY HAVE A KEY ROLE IN NORMAL AND PATHOLOGICAL ACTIONS
OF SECRETORY PHOSPHOLIPASE A2. ALSO BINDS TO SNAKE PA2-LIKE
                                                                  ---PNHSLSSPKEDWVLCRVFHKNTEGVICRDNMGSCFDETASASLPPLMDPYINFDQEP
                                                                                                   121 PLIPEHSGGHPKSDPVAFRPLH-----CPFLLETKILERAPFWVPTCLPPYL----
                                                                                                                                       209 SSYLSDDHHYIINEHVPCFSNLSQNQTLNSNLTNSVSELKIPCKNPNPLFTGGS----AS
                                                                                                                                                                                                        265 ATLTGLDSFCSSDQMVLRALLSQLTKIDGSL-------GPKESQSYGE---G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oryctolagus cuniculus (Rabbit).
Eukaryota, Metazoa, Chordata; Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: Type I membrane protein.
TISSUE SPECIFICITY: LUNG, SKELETAL MUSCLE, BRAIN, KIDNEY AND
                                                                                                                                                                                                                                                                                                                                                                                                                                01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
180 kDa secretory phospholipase A2 receptor precursor (PLA2-R).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-Skeletal muscle;
MEDLINE-94124484; PubMed-8294398;
Lambeau G., Ancian P., Barhanin J., Lazdunski M.;
"Cloning and expression of a membrane receptor for secretory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: CONTAINS 8 C-TYPE LECTIN FAMILY DOMAINS. SIMILARITY: CONTAINS 1 RICIN B-TYPE LECTIN DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                   1458 A.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
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Interpro; IPR000772; Ricin_B_lectin.
Interpro; IPR001304; lectin_c.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U03455; AAC48402.1; -.
                                                                                                                                                                                                                                                                                               307 SSESLL-TDIGIPSTV 321
                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID-9986;
                                                                                                                                                                                                                                                                                                                                                                                                 PA2R_RABIT
P49260;
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110 ILRKGKLVGM----RKTLVFYQ-----GRAPRGRKTDWVMHEFRLQGSHHPPNHS 155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      156 LSSPKEDWVLCRVFHKNTEGVICRDNMGSCFDE--TASASLPPLMDPYIN---FDQEPSS 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                822 YLFYPHSSEWSSFEFVCGWLRSDILTIHSAHEQEFILSKI------KALSKYGAN 870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ------RDRKYATGLRINR----ATATGYWKATGKDRT 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          871 WWIGLOEFTANDELRWRDGTPVIYONWDKERDRSMNNOSORCAFISSITGLWD----- 923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1020 WIGLQNDDYEKWLNGNPVAYSNWSPSDIINIPSYNTTADQKPIPLCALLSSNPNFHFTG 1078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23 FRFHPKDD-----ELVCDYLMR--RSLHNNHRPPLVLIQVDLNKCEPWDIPKMACVGGKD 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               211 YL---SDDHHYIINEHVPCFSNLSQNQTLNSNLTNSVSELK-IP----CKNPNPLFTG 260
                                                                                                              180 KDA SECRETORY PHOSPHOLIPASE A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       . .) (POTENTIAL)
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(POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (POTENTIAL)
                               PROSITE; PS50231; RICIN_B_LECTIN: 1.
Signal; Receptor: Transmembrane; Repeat; Glycoprotein; Lectin.
SIGNAL 1. 23 POTEWIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4.8%; Score 84.5; DB 1; Length 1458; 19.7%; Pred. No. 23;
                                                                                                                                                                                                                                           RICIN B-TYPE LECTIN.

C-TYPE LECTIN 1 (LONG FORM).

C-TYPE LECTIN 3 (LONG FORM).

C-TYPE LECTIN 4 (LONG FORM).

C-TYPE LECTIN 5 (LONG FORM).

C-TYPE LECTIN 6 (LONG FORM).

C-TYPE LECTIN 6 (LONG FORM).

C-TYPE LECTIN 7 (LONG FORM).

C-TYPE LECTIN 7 (LONG FORM).

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N-LINKED (GLCNAC...)
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15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
Hypothetical 38.7 kDa protein C6B12.11 in chromosome I.
                                                                                                                                                                    EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                          CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           337 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          44; Mismatches
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  FIBRONECTIN_2; 1.
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Schizosaccharomyces
PROSITE; PS00023;
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                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its meb by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE-20083488; PubMed-10617198;
MAYOR K.F.X., Schueller C., Wambutt R., Murphy G., Volckaert G.,
Pohl T., Duesterhoeft A., Stiekema W., Entian K.-D., Terryn N.,
Harris B., Ansorge W., Brandt P., Grivell L.A., Rieger M.,
Weichselgartner M., de Simone V., Obermaier B., Mache R., Mueller M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana (Mouse-ear cress).

Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicalesp; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   135 KIDWVMHEFRLQGSHHPPNHSLSSPKEDWVLCRVFHKNTEGVICRDNMGSCFDETASASL 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67 KVDFKFQTPTKQRAETEANESPKAPRNDYL--QVTPKTV-------DKSLLGPT 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         112 POLSRRVLN------LLEDMSPIADSHVDQISDIKHN------TSEISSTMIPTTPS 156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Putative eukaryotic translation initiation factor 3 subunit 7 (eIF-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                               61; Gaps
                                                                                                    Gentles S., Churcher C.M., Barrell B.G., Rajandream M.A., Wood V.; Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 337;
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        DOMAIN
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        232
        POLY-SER.

        SEQUENCE
        337
        AA;
        38684
        MW;
        30A532A8C6322B1C
        CRC64;

   Schizosaccharomycetales; Schizosaccharomycetaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 4.8%; Score 83.5; Di
Best Local Similarity 23.3%; Pred. No. 3.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               49; Conservative 25; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   212 GSNEEKILQEFESFSSSSSESLVDRDISQP 241
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                                                                                                                                                                                                                                                                                                                   EMBL; Z98531; CAB11071.1; -.
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                                                                                                                                                                                                                                                                                                                                        Hypothetical protein.
                      Schizosaccharomyces.
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                                                                      SEQUENCE FROM N.A.
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                                     NCBI_TaxID=4896;
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P56820;
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IF37_ARATH
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Braeken M., Weltjens I., Voet M., Bastiaens I., Aert R., Defoor E., Reitzenegger T., Bothe G., Ramsperger U. Hilbert H., Braun M., RA Holzer E., Brandt A., Peters S., van Staveren M., Dirkse W., Mooijman P., Klein Lankhorst R., Rose M., Hauf J., Koetter P., Bernats S., Hempel S., Feldpausch M., Hambel J., Koetter P., Bernats S., Hempel S., Feldpausch M., Hanber H., De Clercg R., RA Montagu W., Rogers J., Cronin A., Quail M., Bray Allen S., An Montagu W., Rogert J., Hall S., Kay M., Lennard W., McLay K., Mayes R., RA Bucker H., Scharfe M., Grimm M., Lochnart T.-H., Bocker H., Scharfe M., Grimm M., Lochnart T.-H., Rabel C., Fuchs M., Partmann B., Granderath K., Dauner D., Herzl A., RA, Boucker H., Scharfe M., Grimm M., Lochnart T.-H., Assenct O., Quigley F., Clabauld G., Muendlein A., Felber R., Schaal S., Hiller R., Schmidt W., Lecharny A., Aubourg S., RA, Berger C., Wonfort A., Casaucherta E., Ra, Dernann S., Hanger C., Ra, Berger C., Monfort A., Casaucherta E., Ra, Dernann D., Hasse D., Liguori R., Pabermann S., Ra, Perez-Perez A., Purnelle B., Bent E., Johnson S., Tacon D., Josse T., Heijnen L., Schwarz S., Scholler P., Heber S., Francs P., Bielke C., Rannell L., Dedhia N., Wilson R.K., de la Batifed M., Habermann K., Rannell L., Dedhia N., Wilson R.K., de la Batifed M., Johnson D., Ra Arrenille P., Bevan M., Wilson R.K., de la Batifed M., Johnson D., Rannell P., Derdie W., Miller M., Grock T., Kramer J., Fulton L., Mardis E., Andrews S., Geisel C., Layman D., Ryan E., Mank P., Schuler M., Johnson A., Antonoiu B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C., Ramar S., Shoddy N., Hasepsen R., Molth M., Basepsen R., Miller M., Martlenssen R., Marta M., Martlenssen R., Molth M., Basepsen R., Molth M., Martlenssen R., Molth M., Martlenssen R., 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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-!- FUNCTION: BINDS TO THE 40S RIBOSOME AND PROMOTES THE BINDING OF METHIONYL-TRNAI AND MRNA. ASSOCIATES WITH THE SUBUNIT P170 OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein; Initiation factor; Protein biosynthesis. SEQUENCE 591 AA; 66724 MW; 9C5E673F04E9845C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4.8%; Score 83.5; DB 1; Length 591;
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us-09-889-926-2.rsp

Page 12

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                                                                                                                                                                                                275 ILAALMCAPRSVYSWDIVIQRVGNKLFFDKRDGSQLDLLSVHETSQEPLPESKDDINSAH 334
                                                                                                                                                 335 SLGVEAAYINQNFSQQVLVRDGKKETFDEA-----NPFANEGEEIASVAYRYRWK 385
                                                                                                                                                                                                                                                386 LDDNMHLVARCELQSVADLNNQRSFLTLNALNEFDPK7SGVDWRQKLE---TQRGAVLAT 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mouse intracisternal a-particle (IAP-MIAE).
Viruses: Retroid viruses; Retroviridae; Intracisternal A-particles.
-----APR-----GRKTDWVMH---EFRLQGSHHPPNHSLSSPKED----
                                                                                                 163 --WVLCRVFHKN-TEGVICRDNMGSCFDETASASLPPLMDPYINFDQEPSSY-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

MEDLINE-92015460; PubMed=1920613;

Reuss F.U., Schaller H.C.;

"CDNA sequence and genomic characterization of intracisternal
A-particle-related retroviral elements containing an envelope
gene.",
J. Virol. 65:5702-5709(1991).
-!- MISCELLANEOUS: READTHROUGH OF THREE TEHMINATORS OCCURS: UGA
BETWEEN CODONS FOR 71-THR AND 72-ALA, UGA BETWEEN CODONS FOR
111-HIS AND 112-ARG, AND UAA BETWEEN CODONS FOR 394-VAL AND
395-SER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (POTENTIAL).
(POTENTIAL).
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(POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
11-OCT-2001 (Rel. 40, Last annotation update)
ENV polyprotein precursor (Coat polyprotein) [Contains: Surface protein; Transmembrane protein].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL)
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POTENTIAL.
ENV POLYPROTEIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- MISCELLANEOUS: THIS PARTICLE IS A DEFECTIVE RETROVIRUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRANSMEMBRANE PROTEIN. POTENTIAL.
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PIR; A41305; VCMSIA.
Sight protein; Glycoprotein; Polypro
SIGNAL 1 25
                                                                                                                                                                                                                                                                                                    250 PCKNPNPLFTGGSASATLTGLD 271
                                                                                                                                                                                                                                                                                                                                                      443 ELKNNGNKLAKWTAQALLANAD 464
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11;
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                                                                                                                                                                                                                                                                     178 CRDNMGSCFDETASASLPPLM--DPYINFDQEPSSYLSDDHHYIINEHVPCFSNLSQNQT 235
                                                                                                                                                                                                                                                                                                     177 COSSITRWVDOSKTFSFSPNMIDDPEKEFVMKKGLFIQDFRMHPFHKWVLCGVNGS---- 232
                                                                                                                                                                                                                                                                                                                                                                                          261
                                                                                                                                                        Gaps
                                                                                                                                                                                           134 RKIDWVMHEFRLQGSHHPPNHS----LSSPK-----EDWVLCRVFHKNTEGVI---- 177
                                                                                                                                                                                                                                                                                                                                                  236 LNSNLINSVSELKIPCKNPNPL-FTGGSA--SATLTGLDSFCSSDQMVLRALLSQLTKID 292
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
1800CAF8F14A4CD6 CRC64;
                                                                                                                                                    81;
                                                                                                              4.7%; Score 82.5; DB 1; Length 584; 22.2%; Pred. No. 9.9; Live 24; Mismatches 63; Indels 8:
                                                                                                                                                                                                                                                                                                                                                                                    ------CTELNPLIFIQGGAVGKASFTGISRFAQY-----
                                                                                                                                                                                                                                                                                                                                                                                                                            293 GSLGPKESQSYG-----EGSSESLLTDIGIPST 320
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262 WGIHDASQDSYGYINTSVEITGFNKTLVNOINYPST 297
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469 N-
481 N-
501 N-
65024 MW;
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Matches 48; Conservative
469 4
481 4
501 5
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GenCore version 4.5

Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on:

July 15, 2002, 06:57:08; Search time 29.23 Seconds

(without alignments)

1917.563 Million cell updates/sec

Perfect score:
1757
Sequence:
1 METBEEMKESSISMVEAKLP.......EGSSESLLTDIGIPSTVWNC 324

Scoring table:
BLOSUM62
Gapop 10.0, Gapext 0.5

Searched:
562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters:
562222
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
Database : SPTREMBL\_19:\*
1: sp\_archea:\*

Minimum DB seq length: 0 Maximum DB seq length: 2000000000 ase : SPTREMBL\_19:\*
1: sp\_archea:\*
2: sp\_barchea:\*
3: sp\_fungi:\*
4: sp\_human:\*
5: sp\_invertebrate:\*
6: sp\_mammal:\*
7: sp\_mnmal:\*
7: sp\_mnmal:\*
10: sp\_phage:\*
10: sp\_phage:\*
11: sp\_rofant:\*
11: sp\_rofant:\*
12: sp\_rofant:\*
13: sp\_rofant:\*
14: sp\_unclassified:\*
15: sp\_urchas:\*
16: sp\_archas:\*
17: sp\_archas:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		dФ				
Result No.	Score	Query Match	Query Match Length DB	DB	ID	Description
1	1757	100.0	! !	10	Q9SE10	Q9sel0 arabidopsis
7	1579.5	89.9		10	65868	Q9sgs9 arabidopsis
٣	987	56.2		10	09LS11	Q91sil arabidopsis
4	946	53.8	299	10	093XA7	Q93xa7 phaseolus v
5	557	31.7		10	Q9FLR3	Q9flr3 arabidopsis
9	552.5	31.4		10	040880	Q40880 petunia hyb
7	548	31.2		10	Q9FLJ2	Q9flj2 arabidopsis
80	545.5	31.0		10	Q9FK44	
6	544	31.0		10	004017	
10	542	30.8		10	095068	Q9sc68 oryza sativ
11	542	30.8		10	06 <b>W</b> 860	_
12	536.5	30.5		10	095851	Q9s851 arabidopsis
13	535.5	30.5		10	09LS50	Q91s50 arabidopsis
14	533	30.3		10	о в при	Q9ljw3 arabidopsis
15	532.5	30.3		10	900860	Q9sqq6 arabidopsis
16	519	29.5		10	09FKA0	Q9fka0 arabidopsis

O96rv4 arabidopsis O9frv4 arabidopsis O92425 arabidopsis O95425 arabidopsis O96740 oryza sativ O96741 arabidopsis O9772 triticum sp O98171 arabidopsis O9689 arabidopsis O9784 arabidopsis O9080 arabidopsis O9080 arabidopsis O9103 arabidopsis O9103 arabidopsis O91041 arabidopsis O991041 arabidopsis O991041 arabidopsis O991041 arabidopsis O99108 arabidopsis	Q9fiw5 arabidopsis Q91sh5 arabidopsis Q948z2 solanum tub Q9znu2 arabidopsis Q91pi7 arabidopsis Q9ffi5 arabidopsis
09AV06 09FRV4 095LILB 095LILB 095LILB 095RZ2 095RZ2 095RZ2 095RZ3 095RZ3 095RZ3 095RZ3 095RZ3 095RZ4 091DX8	Q9FIW5 Q9LSH5 Q948z2 Q9zNU2 Q9LPI7
	100 100 100 100
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-	25.3 25.2 25.0 25.0 25.0 24.9
512 512 512 512 65.5 65.5 74.5 74.5 74.5 74.5 74.5 74.5 74.5 7	444 442 439.5 439 438.5 437.5
	4444 444 443

## ALIGNMENTS

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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Khan S., Kim C., Altafi H., Bei Q., Chin C., Chiou J., Choi E., Conn L., Conway A., Gonzales A., Hansen N., Howing B., Koo T., Lam B., Lee J., Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N., Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A., Toriumi M., Vaysberg M., Yu G., Federspiel N.A., Theologis A., Ecker J.R.)
                                                                                                                                                   Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genomic sequence for Arabidopsis thaliana BAC F14J16 from chromosome
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SEQUENCE FROM N.A.
STRAIN=CV. LANDSBERG;
Xie Q., Chua N.H.;
"Arabidopsis NAC1 transduces auxin signal to promote later root
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ecker J.R.; Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                 development.";
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases
                                                    01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                               324 AA
                                PRT;
                                PRELIMINARY;
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                                                   Q9SE10;
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Best Local Similarity 91.8
Matches 302; Conservative
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                                                                                                                                Cheuk R., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Khan C., Altafi H., Bei B., Chin C., Chiou J., Choi E., Conn L., Conway A., Ganzalez A., Hansen N., Howing B., Koo T., Lam B., Lee J., Lenz C., Li J., Liu A., Liu J., Liu S., Mukharsky N., Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N., Theologis A., Ecker J.; Submitted (JUN-2000) to the EMBL/GenBank/DibJ databases.

EMBL, AR1980644 AAF19128.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                            61 EPWDIPKMACVGGKDWYFYSQRDRKYATGLRINRATAIGYWKATGKDRIILRKGKLVGMR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 EPWDIPKMACVGGKDWYFYSQRDRKYATGLRINRATAIGYWKATGKDRTILRKGKLVGMR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 KTLVFYQGRAPRGRKTDWVMHEFRLQGSHHPPNHSLSSPKEDWVLCRVFHKNTEGVICRD 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                           ;
0
                                                                                                                                                                                                                                                                                                                                  100.0%; Score 1757; DB 10; Length 324; 100.0%; Pred. No. 6.7e-161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. Federspiel N.A., Palm C.J., Conway A.B., Conn L., Hansen N.F.,
                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                             Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
               to the EMBL/GenBank/DDBJ databases.
                                                             to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                              36569 MW; C70ED705D1A06957 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
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                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.
Matches 324; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                 Pfam; PF02365; NAM; 1.
Ecker J.R.;
Submitted (AUG-1997)
                                                             Submitted (APR-2000)
                                    SEQUENCE FROM N.A.
                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                              SEQUENCE
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Q9SGS9;
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Altafi H., Nguyen M., Lam B., Buehler E., Dunn P., Gonzalez A., Kremenetskaia I., Kim C., Lenz C., Li J., Liu S., Luros S., Schwartz J., Shinn P., Toriumi M., Vysotskaia V.S., Walker M., Yu G., Ecker J., Theologis A., Davis R.W., Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AC009894; AAF02847.1; -
InterPro; IPR003441; NAM.

Pfam; PF02365; NAM; 1.

SEQUENCE 309 AA; 34715 MW; 2A263CD213E44688 CRC64;

    Sequence
    and TAC

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  116 LVGMRKTLVFYQGRAPRGRKTDWVMHEFRLQGSHHPPNHSLSSPKEDWVLCRVFHKNTEG 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2000 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
NAM (NO APICAL MERISTEM) PROTEIN-LIKE.
Arabidopsis thaliana (Mouse-ear cress)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 EPWDIP-----KMACVGGKDWYFYSQRDRKYATGLRTNRATATGYWKATGKDRTILRKGK 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 EPWDIPMYNTTKRVCV------QRDRKYATGLRINRATATGYWKATGKDRTILRKGK 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        236 LNSNLTNSVSELKIPCKNPNPLFTGGSASATLTGLDSFCSSDQMVLRALLSQLTKIDGSL 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 METEEEMKESSISMVEAKLPPGFRFHPKDDELVCDYLMRRSLHNNHRPPLVLIQVDLNKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           176 VICRDNMGSCFDETASASLPPLMDPYINFDQEPSSYLSDDHHYIINEHVPCFSNLSQNQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Tabata S.; Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                     DB 10; Length 309;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Structural analysis of Arabidopsis thaliana chromosome 3. I features of the regions of 4,504,864 bp covered by sixty Pl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA Res. 7:131-135(2000).

EMBL; AB026645; BAB02506.1; -.

INTERPRO; IPRO3441; NAM.

PÉAM; PF02355; NAM; 1.

SEQUENCE 279 AA; 31946 MW; 376EEE552927C416 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                  89.9%; Score 1579.5; DB 10.01.8%; Pred. No. 7.8e-144; ive 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   279 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GPKESQSYGEGSSESLLTDIGIPSTVWNC 324
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O40880; Q40894;
01-NOV-1996 (TrEMBLrel. 01, Created)
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                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                        MEDLINE=98290546; PubMed=9628582;
                                                           305 EGSSESLLTDIGIPSTVWN 323
                                                                         280 EGSSESYLSEVGMPH-MWN 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best_Local Similarity 42.29
Matches 127; Conservative
                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                              STRAIN-COLUMBIA;
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Q40880
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Q9FLR3
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                                                                                                                                                                                                                                                 ---ASPDQMILRTLLSQLTK----KVEES 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DIPKMACVGGKDWYFYSQRDRKYATGLRTNRATATGYWKATGKDRTILRKGKLVGMRKTL 123
                                                                                                         VFYQGRAPRGRKTDWVMHEFRLQGS--HHPPNHSLSSPKEDWVLCRVFHKNTEGVICRDN 181
                                                                                                                                                     178 TRSCSDATASA----FMDSYINF-----DHHHIINOHVPCFSNNLSHNOTNOSGL 223
                                                                                                                                                                                                                                                                                                                                                                                                                                     Phaseolus vulgaris (Kidney bean) (French bean).
Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta:
Spermatophyta: Magnoliophyta: eudicotyledons; core eudicots; Rosidae;
eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Phaseolus.
NCBI_TaxID=3885;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CVGGKDWYFYSQRDRKYATGLRTNRATATGYWKATGKDRTILRKGKLVGMRKTLVFYQGR 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                130 APRGRKTDWVMHEFRLQGSHHPPNHSLSSPKEDWVLCRVFHKNTEGVICRDNMGSCFDET 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      119 APKGRKTEWVMHEFRIEGPHGPP--KVSSSKEDWVLCRVFYKSRE-VSAKPSMGSCYEDT 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               190 ASASLPPLMDPYINFDQEPSSYLSDDHHYIINEHVPCFSNLSQNQT--LNSNLTNSVSEL 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   50; Gaps
                                              4 EEEMKESSISMVEAKLPPGFRFHPKDDELVCDYLMRRSLHNNHRPPLVLIQVDLNKCEPW 63
                                                                     61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               55; Indels 28; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SSISMVEAKLPPGFRFHPKDDELVCDYLMRRSLHNNHRPPLVLIQVDLNKCEPWDIPKMA 69
                                                          182 MGSCFDETASASLPPLMDPYINFDQEPSSYLSDDHHYIINEHVPCFS-NLSQNQTLNSNL
                                                                                                                                                                                                                                    241 TNSVSELKIPCKNPNPLFTGGSASATLTGLDSFCSSDQMVLRALLSQLTKIDGSLGPKES
 Length 279;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      53.8%; Score 946; DB 10; Length 299; 60.2%; Pred. No. 7.3e-83; Live 44; Mismatches 55; Indels 2
                         Indels
                                                                                                                                                                                                                                                                                                                                                                                       01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
NAC DOMAIN PROTEIN NACI.
                         46;
56.2%; Score 987; DB 10; 62.8%; Pred. No. 7.5e-87;
                                                                                                                                                                                                                                                                                                                                                                   299 AA.
                       24; Mismatches
                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                301 QSYGEGSSESLLTDIGIPSTVWN 323
                                                                                                                                                                                                                                                                                                       256 QSRGDGSSESQLTDIGIPSHAWN 278
                                                                                                                                                                                                                                                         224 IS------KNSSPLFN-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best_Local Similarity 60.2%
Matches 192; Conservative
                       Matches 203; Conservative
                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
             Similarity
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 Query Match
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              Best Local
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01-MAR-2001 (TrEMBLrel. 16, Created).
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
NAM (NO APICAL MERISTEM)-LIKE PROTEIN.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota: Viridiplantae: Streptophyta: Embryophyta; Tracheophyta; Spermatophyta: Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                     229 -----PATTYGGAPNLGYCLDPL-SCDRKVLKAVLSQITKMERNPLNQSLKGSTSFG 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62 PWDIPKMACVGGKDWYFYSQRDRKYATGLRTNRATATGYWKATGKDRTILRKGKLVGMRK 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59 PWELPYKAKIGEKEWYFFCVRDRKYPTGLRTNRATQAGYWKATGKDKEIFRGKSLVGMKK 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  122 TLVFYQGRAPRGRKTDWVMHEFRLQG---SHHPPNHSLSSPKEDWVLCRVFHKNTEG--- 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  119 TLVFYRGRAPKGOKTNWVMHEYRLDGKLSAHNLP----KTAKNEWVICRVFHKTAGGKKI 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             176 -VICRDNMGSCFDETASASLPPLMD--PYINFDQEPSSYLSDDHHYIINEHVPCFSNLSQ 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          220 TRGTILNCFSNPSLSSIQPDFLQMIPLYQPQSLNISESSNPVLT-----QEQSVLQAM 272
248 KIPCKNPNPLFTGGSASATLTGLDSFCSSDQMVLRALLSQLTKIDG---SLGPKESQSYG 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Structural analysis of Arabidopsis thaliana chromosome 5. IV. Sequence features of the regions of 1,456,315 bp covered by nineteen physically assigned Pl and TAC clones."; DNA Res. 5:41-54(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 ETEEEMKESSISMVEAKLPPGFRFHPKDDELVCDYLMRRSLHNNHRPPLVLIQVDLNKCE 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sato S., Kaneko T., Kotani H., Nakamura Y., Asamizu E., Miyajima
Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        54;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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INLECTPO; IPR003441; NAM.
PFam; PFC2355; NAM; 1.
SEQUENCE 329 AA; 37517 MW; 8211824FD93933EC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31.7%; Score 557; DB 10;
42.2%; Pred. No. 2.4e-45;
tive 42; Mismatches 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                327 AA.
                                                                                                                                                                                                                                                                                                                                                                                            329 AA.
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NCBI_TaxID=3702;
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                                          STRAIN-COLUMBIA;
                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9FK44;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               188 -----ETASASLPPLAD--PYINFDQEPSSYLSDDHHYIINEHVPCFSNL----- 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae; Streptophyta; Emkryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                76 WYFYSQRDRKYATGLRTNRATATGYWKATGKDRTIL--RKGKLVGMRKTLVFYQGRAPRG 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        134 RKTDWVMHEFRLQGSHHPPNHSLS-SPKEDWVLCRVFHKNTEGVICRDNMG-----SCFD 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 130 EKSNWVMHEYRLDGKF--AYHYISRSSKDEWVISRVFCKSCSTVGTTSNGGKKRLNSSFN 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           188 NMYOEVSSPSSVSLPPLLESSPYNN--TATSAAASK-----KEHVSCFSTISTPSFDPS 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16 EAKLPPGFRFHPKDDELVCDYLMRRSLHNNHRPPLVLIQVDLNKCEPWDIPKMACVGGKD 75
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                                                      Petunia hybrida (Petunia).
Sukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledors; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Petunia.
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                                                                                                                                                                                   Souer E., van Houwelingen A., Kloos D., Mol J., Koes R.; The no aptical meristem gene of Petunia is required for pattern formation in embryos and flowers and is expressed at meristem and primordia boundaries.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31.4%; Score 552.5; DB 10; Length 327; 42.8%; Pred. No. 6.3e-45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               69; Indels
                                                                                                                                                                                                                                                                                                     Souer E.J.; Submitted (OCT-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                      Souer E.J.;
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                          94C428A0176A8B3E CRC64;
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01-MAR-2001 (TrEWBLrel. 16, Created)
01-MS-2001 (TrEWBLrel. 16, Last sequence update)
01-DEC-2001 (TrEWBLrel. 19, Last annotation update)
 01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                         STRAIN-W137, AND W138; TISSUE-LEAF, AND CAEPEL; MEDLINE-96200768; PubMed-8612269;
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                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR003441; NAM.
Pfam; PF02365; NAM; 1.
SEQUENCE 327 AA; 36788 MW;
                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; X92204; CAA63101.1; -. EMBL; X92205; CAA63102.2; -.
                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN-W138; TISSUE-CARPEL;
                                                                                                                                                                                                                                                                                      STRAIN-W138; TISSUE-CARPEL;
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                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                NCBI_TaxID=4102;
                             NAM GENE.
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Southwick A., Karlin-Neumann G., Nguyen M., Lam B., Miranda M., Southwick A., Karlin-Neumann G., Nguyen M., Lam B., Miranda M., Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H., Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J., Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H., Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K., Ecker J., Theologis A., Davis R.W.; Submitted (Aug-2001) to the EMBL/GenBank/DDBJ databases.

EMBL, ABO10073; BAB084991; --

EMBL, ABO10073; BAB084991; --

EMBL, AROSEGGA, AAROSES I; --
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MAM (NO APICAL MERISTEM).-LIKE PROTEIN.
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales, Brassicaceae, Arabidopsis.
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                                                                      "Structural analysis of Arabidopsis thaliana chromosome 5. IV. Sequence features of the regions of 1,456,315 bp covered by nineteen physically assigned Pl and TAC clones.";
DNA Res. 5:41-54(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         101; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            38472 MW; 2595C4FBBD8B0680 CRC64;
                     Sato S., Kaneko T., Kotani H., Nakamura Y., Asamizu
Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31.2%; Score 548; DB 10; 37.3%; Pred. No. 1.8e-44;
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MEDLINE=98290546; PubMed=9628582;
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Best Local Similarity 37.34
Matches 137; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR003441; NAM.
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SEQUENCE 336 AA; 3:
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NCBI_TaxID=3702;
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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EMBL; AJ243961; CAB51838.1; -.
InterPro; IPR003441; NAM.
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35.5%; Pred. No. 6.6e-44;
tive 41; Mismatches 93;
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Best Local Similarity
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Q9SC68;
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Matches
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MEDLINE=97355980; PubMed=9212461;
Aida M., Ishida T., Fukaki H., Fujisawa H., Tasaka M.;
"Genes involved in organ separation in Arabidopsis: an analysis of the cup-shaped cotyledon mutant.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Sperimatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBL_TaxID-3702;
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MEDLINE=98162728; PubMed=9501997;
Nakamura Y., Sato S., Kaneko T., Kotani H., Asamizu E., Miyajima N.,
                                                                                                                                     Kotani H., Nakamura Y., Sato S., Asamizu E., Kaneko T., Miyajima N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tabata S.;
"Structural analysis of Arabidopsis thaliana chromosome 5. III.
                                                                                                                                                                                               "Structural analysis of Arabidopsis thaliana chromosome 5. VI. Sequence features of the regions of 1,367,185 bp covered by 19 physically assigned Pl and TAC clones.";
DNA Res. 5,203-216(1998).
EMBL: AB012246; BAB09485.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match 31.0%; Score 545.5; DB 10; Length 335; Best Local Similarity 38.7%; Pred. No. 3.1e-44; Matches 122; Conservative 53; Mismatches 87; Indels 53;
                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF02365; NAM; 1.
SEQUENCE 335 AA; 38271 MW; 6B8CF20E10CD68AF CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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01-JUL-1997 (TrEMBLrel. 04, Last seq
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                                                             STRAIN-COLUMBIA;
MEDLINE-98403884; PubMed-9734815;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                290 KIDGSLGPKESQSYG 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        :: | || | |
299 EV--SSGPVMKQEMG 311
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                                    SEQUENCE FROM N.A.
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                                                                                                                                                                         Tabata S.;
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Sequence features of the regions of 1,191,918 bp covered by seventeen physically assigned P1 clones.";
DNA Res. 4:401-414(1997).
EMBL; AB002560; BAA19529.1; -
EMBL; AB007644; BAB10725.1; -
InterPro; IFR003441; NAM.
Pfam; PF02365; NAM; 1.
SEQUENCE 375 AA; 41434 MW; DA2E8AD98F83D11B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              135 KTDWVMHEFRLQGSHHPPNHSLS-SPKEDWVLCRVFHKNT------EG------ 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             74 YFFSLRDRKYPTGLRTNRATEAGYWKATGKDREIFSSKTCALVGMKKTLVFYKGRAPKGE 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               251 VTASAITEHVSCFSTVPTTTTALGLDVNSFSRLPPPLGFDFPPFPFFVSRNVS-TQSNFR 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            77 YFYSQRDRKYATGLRINRATATGYWKATGKDRTIL--RKGKLVGMRKTLVFYQGRAPRGR 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               218 ---YIINEHVPCFSNLSQNQTLNSNLTNSVSELKIPCK---NPNPLFTGGSASATLTGLD 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67 -------KMACVGGKDWYFYSQRDRKYATGLRINRATATGYWK 102
                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                17 LPPGFRFHPTDEELITHYLLRKVLDGCFSSR---AIAEVDLNKCEPWQLPGRAKMGEKEW 73
                                                                                                                                                                                                                                                                                                                                                                                                            19 LPPGFRFHPKDDELVCDYLMRRSLHN--NHRPPLVLIQVDLNKCEPWDIPKMACVGGKDW 76
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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                                                                                                                                                                                                                                                                                                Length 375;
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                                                                                                                                                                                                                                                                                          31.0%; Score 544; DB 10; Length 3 38.5%; Pred. No. 5e-44; Live 38; Mismatches 102; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            272 SFCSSDQMVLRALLSQLTKIDGSLGPKESQSYGEGSSESLLTDIGIPS 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PF02365; NAM; 1.
NCE 331 AA; 36023 MW; 6A2FF50AC9DEF10A CRC64;
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01-JUN-2010 (TrEMBLrel. 17, Las
NYPOTHETICAL 38.0 KDA PROTEIN.
F1466.2 OR F15M4.8
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                                        308 SESLLTDIGIPSTVWN 323
                                                                    ---YVQQSAMASQAWN 329
                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                    STRAIN-CV. COLUMBIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                        098851
                                                                                                             RESULT 12
              292
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                                                                                                 181 DHPSSSTSSSSSNLLKEDWVLCRVFYKSRTANPRPVVSGEAAVSLSGELSLPPPPPLPVA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57 ELPAYFLHNLIIFPARARARARAGRRRRADAARVGATEAYFFSLHDRKYATGQRTNRATRS 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          148 ---SHHPPNHSLSSP----KEDWVLCRVFHK----NTEGVICRDNMGSCFDETASASLPP 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       237 LPVAPAVIDGYTGGYYEQDSSAGCHHHHRRPPTSAALPFKDLTDFRDLLSNWVQ----- 291
61 YFLHNLIIFPARARAAGRRRRADAARVGATEWYFFSLHDRKYATGORTNRATRSGYWK 120
                             ATGKDRTILRK------GKLVGMRKTLVFYQGRAPRGRKTDWVMHEFRLQG---S 148
                                                       121 ATGKDRAIVTRRRAAGGEAVAGGEVVGMRKTLVFYQGRAPRGSKTEWVMHEFRVDGHAVA 180
                                                                                  HHPPNHSLSSP----KEDWVLCRVFHK----NTEGVICRDNMGSCFDETASASLPPL--- 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99 GYWKATGKDRTILRK-----GKLVGMRKTLVFYQGRAPRGRKTDWWHEFRLQG 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      197 L-----MDPYIN---FDQEPSSYLSDDHHYIINEHVPCFSNLSQNQTLNSNLTNSVSEL 247
                                                                                                                                        198 ---MDPYIN---FDQEPSSYLSDDHHYIINEHVPCFSNLSQNQTLNSNLTNSVSELKIPC 251
                                                                                                                                                                                                252 KNPNPLFTGGSASATLTGLDSFCSSDQMVLRALLSQLFKIDGSLGPKESQSYGEGSSESL 311
                                                                                                                                                                                                                        292 ------GGGAAAAAKSEGF-----Y 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---KMACVGGKDWYFYSQRDRKYATGLRTNRATAT 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          177 HAVADHPSSSTSSSSNLLKEDWVLCRVFYKSRTANPRPVVSGEAAVSLSGELSLPPPPP
                                                                                                                                                                 241 PAVIDGYTGGGYYEQDSSAGCHHHHHRPPTSAALPFKULTDFRDLLSNMVQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 331;
                                           STRAIN-CV. INDICA;
Hong G., Zhao W.;
"Oryza sativa genomic DNA, chromosome 4, clone: b6015.";
Submitted (AUG-1999) to the EMBL/GenBank/DJBJ databases.
EMBL; ALL17264; CAB55403.1; -.
InterPro; IPR003441; NAM.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30.8%; Score 542; DB 10;
35.1%; Pred. No. 6.6e-44;
iive 41; Mismatches 89;
                                                                                                                                                                                                                                                                                                                                                    331 A.A.
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SEQUENCE 331 AA; 35
                                                                                                                                                                                                                                                    312 LTDIGIPSTVWN 323
                                                                                                                                                                                                                                                                              318 VQQSAMASQAWN 329
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=4530;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 132;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             190 NHSLSTTHHHHHEALPLLIEPSNKTLTNF----PSLLYDDPH------ONYNNNF 235
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O
248 KIPCKNPNPLFTGGSASATLTGLDSFCSSDQMVLRALLSQLTKIDGSLGPKESQSYGEGS 307
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19 ERGLPPGFRFHPTDEELITFYLASKIFHGG-LSGIHISEVDLNRCEPWELPEMAKMGERE 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.J., Wu Maiti R., Ronning C.M., Koo H., Fujii C.Y., Utterback T.R., Barnstead M.E., Bowman C.L., White O., Nierman W.C., Fraser C.M.; Rarabidopsis thaliana chromosome 1 BAC F1466 genomic sequence."; Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
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Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.,

Ronning C.M., Koo H., Fujil C.Y., Utterback T.R., Barnstead M.E.,

Bowman C.L., White O., Nlerman W.C., Fraser C.M.;

"Arabidopsis thaliana chromosome I BAC F14G6 genomic sequence.";

Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AC012494; AAF16659.1; -.
                                                                       ---HTGMSEEESSG---
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Best Local Similarity 38.3%; Pred. No. 2.3e-43;
Matches 123; Conservative 44; Mismatches 67; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Interpro; IPR003441; NAM.
Pfam; PF02365; NAM; 1
SEQUENCE 334 AA; 38017 MW; 008EF8F3F3220F07 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
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"Structural analysis of Arabidopsis
Sequence features of the regions of
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                                                                                                                                              TAC and BAC clones.";

DNA Res. 7:217-221(2000).

BERL; AP000388; BAB02945.1;

EMBL; AB025615; BAB02945.1;

Interpro; IPR003441; NAM.
                                                                                               MEDLINE=20363099; PubMed=10907853;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 295 LGPKESQSYGEGSSESLLT 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          283 L-----HNSGSSESELT 294
                                                                                                                                                                                                                                                             Query Match 30.35
Best Local Similarity 41.75
Matches 133; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                       SEQUENCE FROM N.A.
[1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                       STRAIN-COLUMBIA;
                                                                                     STRAIN-COLUMBIA;
                                                                                                             Nakamura Y.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DCZ-2001 (TrEMBLrel. 19, Last annotation update)
NAM (NO APICAL MENSTEM) LIKE PROTEIN.
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          185 CFDETASASLPPLMD-----PYINFDQEPSSYLSDDHHYIINEHVPCFSNLSQNQTLNSN 239
                                                                                                                                     Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae, eurosids II; Brassicales, Brassicaceae, Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          75 DWYFYSQRDRKYATGLRINRATATGYWKATGKDRTILRKGKLVGMRKTLVFYQGRAPRGR 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15 VEAKLPPGFRFHPKDDELVCDYLMRRSLHNNHRPPLVLIQVDLNKCEPWDIPKMACVGGK 74
                                                                                                                                                                                                                             S:
                                                                                                                                                                                                                                                                                                                                                                                                                                       30.5%; Score 535.5; DB 10; Length 314; 45.0%; Pred. No. 2.6e-43; Live 37; Mismatches 75; Indels 25;
                                                                                                                                                                                                                          Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Tabata Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                    DNA Res. 7:131-135(2000).

EMBL; AB026658; BAB01106.1; -.

INTECTPO: IPR03441; NAM.

PÉDRI; PP02355; NAM; 1.

SEQUENCE 314 AA; 35745 MW; 2D4AFCEFBE319580 CRC64;
                                                                                                  01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                       Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  318 AA
                                                   314 AA.
                                                                                                                            Arabidopsis thaliana (Mouse-ear cress).
                                                                          01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last seq
                                                   PRT;
                                                                                                                                                                                                                                                                             STRAIN-COLUMBIA;
MEDLINE=20277480; PubMed=10819329;
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Matches 112; Conservative
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                                                   PRELIMINARY;
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                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                               SIMILARITY TO NAM.
                                                                                                                                                                                                                 STRAIN-COLUMBIA;
                                                                                                                                                                            NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                      Nakamura Y.;
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                                                                Q9LS50;
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                                                   09LS50
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                           RESULT 13
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13;
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4,251,695 bp covered by ninety Pl,
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.

NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        229 SLVADFK-----TTMFGSGSTNFLPNIGSLLDFDPLFLQNNSSVLKMLLDNEETQFKKN 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64 DIPKMACVGGKDWYFYSQRDRKYATGLRINRATATGYWKATGKDRTILRKGKLVGMRKTL 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    124 VFYQGRAPRGRKTDWVMHEFRLQGSHHPPNHSLSSPKEDWVLCRVFHKNTEGVICRDNMG 183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      180 ---KEHMSVGLPPLMDSSPYLKSRGQDS--LAGTTLGGLLSHVTYFS----DQTTDDK-- 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      242 NSVSELKIPCKNPNPLFTGGSAS----ATLTGLDS-FCSSDQMVLRALL-SQLTKIDGS 294
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Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.,
Ronning C.M., Koo H., Fujii C.Y., Utterback T.R., Barnstead M.E.,
Bowman C.L., White O., Nierman W.C., Fraser C.M.;
"Arabidopsis thaliana chromosome III BAC T11118 genomic sequence.";
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
   Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        46;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UN-2001 (TrEMBLrel. 17, Last annotation update)
NAM-LIKE PROTEIN (NO APICAL MERISTEM) (AT3G04060/T11118_17)...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 318;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
Kaneko T., Kato T., Sato S., Nakamura Y., Asamizu E., Te
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF02365; NAM; 1.
SEQUENCE 318 AA; 35825 MW; 67EE3AlDE4F33C93 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30.3%; Score 533; DB 10;
41.7%; Pred. No. 4.6e-43;
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12;
              A Shinn P., Chen H., Cheuk R., Kim C.J., Banin J., Bowser L.,
A Carninci P., Chung M.K., Goldsmith A.D., Hayashizaki Y., Ishida J.,
A Carninci P., Chung M.K., Goldsmith A.D., Hayashizaki Y., Ishida J.,
A Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B., Lee J.M.,
Lin J., Liu S.X., Miranda M., Narusaka M., Nguyen M., Palm C.J.,
A bham P.K., Quach H.L., Sakano H., Sakurai T., Satou M., Seki M.,
Southwick A., Toriumi M., Yamada K., Yu G., Shinozaki K., Davis R.W.,
Theologis A., Ecker J.R.;
Submitted (WAR-2001) to the EMBL/GenBank/DDBJ databases.
RMBL, AC011698; AAR37911; -
RMBL, AR561623; AAR37911; -
R InterPro; IPRO2441; NAM.
R Pfam; PF02565; NAM; 1.
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197 LD---FSSLPPLIDPGFLGQPGPSFSGARQQHDLKPVLHHPTTAPVDNTYLPTQALNFPY 253
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                217 HYIIN-----TUSVSELKIPCKNP 254
                                                                                                                                                                                                                                                                                                                                           Query Match 30.3%; score 532.5; DB 10; Length 338; Best Local Similarity 39.4%; Pred. No. 5.6e-43; Matches 125; Conservative 43; Mismatches 76; Indels 73; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | : | : | : | : | : | : | 34 HSVHNSGSDFGYGAGSGNNNKGMIKLEH~-SLVSVSQETGLSSDVNTTATPEISSYPMMM 311
                                                                                                                                                                                                                                                                                                                                                                                                                         19 LPPGFRFHPKDDELVCDYLMRRSLHNNHRPPLVLIQVIXLNKCEPWDIPKMACVGGKDWYF 78
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SEQUENCE FROM N.A.
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
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Gapop 10.0 , Gapext 0.5
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111: /SIDSI/gcgdata/hold-geneseqy-embl/AA1989.DAT:\*
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113: /SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1989.DAT:\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

					SUMMARIES		
Result No.	Score	% Query Match	å Query Match Length DB	DB	ΙD	Description	
	1757	100.0	324	21		Arabidopsis	NAC1 p
7	1561	88.8		21	AAG22847	Arabidopsis	thalia
9	1391	79.2		21	AAG17253	Arabidopsis	thalia
4	1391	79.2		21	AAG22848	Arabidopsis	+
5	1112	63.3		21	AAG17254	Arabidopsis	thalia
9	1112	63.3		21	AAG22849	Arabidopsis	+
7	1112	63.3		21	AAG45796	Arabidopsis	u
۵	1112	63.3		21	AAG45825	Arabidopsis	-
6	997	56.7		21	AAG17255	Arabidopsis	thalia
10	997	56.7	185	21	AAG45797	Arabidopsis	thalia
11	66	56.7		21	AAG45826	Arabidopsis	thalia

Isolated NAC1 gene sequence from Arabidopsis thaliana is used to produce transgenic plants which are larger than the wild type versions

N-PSDB; AAA89936

Claim 2; Page 20-21; 35pp; English.

s thali	Arabidopsis challa	s thali	s thali	ß	Ø	S	Ø	ι	is			to.		Arabidopsis thalia	is	G	o.	is	O	Ø	is		Ω		tha		ivir				Wheat geminivirus	
279	AAG4582/	7 4	27	13	999	AAG46673	AAG17129	67	AAG25574	AAG27013	59	57	59	47	AAG25575	AAG27014	AAG46691	AAG21814	AAE02527	AAG53465	AAG46921	AAE02484	51	AAE02512	AAG16952	AAG13616	29	29		m	AAW88294	$\overline{}$
21	7 6	7 7	21	21	21	21	21	21	21	21	21	21	21	22	21	21	21	21	22	21	21	22	21	22	21	21	20	21	21	21	20	21
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## ALIGNMENTS

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NAC 1; genetically modified; larger.
                                                                                                                                             (MOLE-) INST MOLECULAR AGROBIOLOGY.
           AAB15081 standard; Protein; 324 AA
                                                                                                                                 99WO-SG00011.
                                                                                                                    99WO-SG00011.
                                      19-DEC-2000 (first entry)
                                                    Arabidopsis NAC1 protein.
                                                                             Arabidopsis thaliana.
                                                                                                                                                                         WPI; 2000-506095/45.
                                                                                                                                                            Xie Q, Chua N;
                                                                                          WO200047742-A1.
                                                                                                                                 11-FEB-1999;
                                                                                                                    11-FEB-1999;
                                                                                                       17-AUG-2000.
                         AAB15081;
RESULT
AAB15081
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The present sequence is Arabidopsis thaliana NAC1 protein. The NAC1 gene belongs to the NAC family of genes which may play a role in patterning of the shoot and floral meristem. This gene was isolated from an A. thaliana cDNA library expressed in Schizosaccharomyces pombe cells. The NAC1 gene may be used for making a genetically altered plant which is larger than a wild type version of the plant by overexpressing NAC1. The modified plant produces larger leaves, larger roots and more lateral roots than the wild type version.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein identification; signal transductior pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                                                                                                                                                                      240
                                                                                                                                                                                                                                                                                                                                                                                                                                           EPWDIPKMACVGGKDWYFYSQRDRKYATGLRTNRATATGYWKATGKDRTILRKGKLVGMR 120
                                                                                                                                                                                                                                                                                                                           KTLVFYQGRAPRGRKTDWVMHEFRLQGSHHPPNHSLSSPKEDWVLCRVFHKNTEGVICRD 180
                                                                                                                                                                                              0; Gaps
                                                                                                                                                                                                                                     1 METEEEMKESSISMVEAKLPPGFRFHPKDDELVCDYLMRRSLHNNHRPPLVLIQVDLNKC 60
                                                                                                                                                                                                                                                                                                                                                                           241 TNSVSELKIPCKNPNPLFTGGSASATLTGLDSFCSSDQMVLRALLSQLTKIDGSLGPKES
                                                                                                                                                                   100.0%; Score 1757; DB 21; Length 324; 100.0%; Pred. No. 5.6e-172; Live 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana protein fragment SEQ ID NO: 25931.
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990S-0123180.
990S-0125788.
990S-0125788.
990S-0126785.
990S-0126785.
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                                                                                                                                                                                              Matches 324; Conservative
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                                                                                                                                                                                 Similarity
                                                                                                                                324 AA;
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29-MAR-1999;
01-APR-1999;
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09-MAR-1999;
23-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                     TGYWKATGKDRTILRKGKLVGMRKTLVFYQGRAPRGRKTDWVMHEFRLQGSHHPPNHSLS 157
                                                                                                                                                                                                                                                                     0; Gaps
                                                                                                                                                                                                                                   Length 287;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana protein fragment SEQ ID NO: 18203.
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14-0CT-1999;
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Arabidopsis thaliana
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01-JUN-1999;
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                    EP1033405-A2
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30-APR-1999;
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AAG17254 standard; Protein; 206 AA.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TLVFYQGRAPRGRKTDWVMHEFRLQG---SHHPPNHSLSSPKEDWVLCRVFHKNTEG--- 175
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                                                                                                                                                                                                                                                                                                                                                                                                                   31.7%; Score 557; DB 21; Length 329; 42.2%; Pred. No. 1.5e-48; tive 42; Mismatches 78; Indels 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana protein fragment SEQ ID NO: 58726.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAG46660 standard; Protein; 329 AA.
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990S-0123180.
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990S-0126264.
                                                       99US-0160980.
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Matches 127; Conservative
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05-MAR-1999;
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16-OCT - 1999;

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Search completed: July 15, 2002, 06:56:42 Job time: 229 sec

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GenCore version 4.5

Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on:

July 15, 2002, 06:54:48; Search time 13.14 Seconds

(without alignments)
602.275 Million cell updates/sec

Title:

US-09-889-926-2

Sequence:

1757

Sequence:

Scoring table:

Gapop 10.0, Gapext 0.5

Searched:

231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters:

231628
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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: Issued\_Patents\_AA:\*

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4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep:\*
5: /cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep:\*
6: /cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		d			SUMMARIES	
Result No.	Score	Query Match	Length	DB	ID	Description
	106	6.0	1872	-	US-08-188-582-14	Sequence 14, Appl
8	106	6.0	1872	Н	US-08-646-715-14	Sequence 14, Appl
m	106	0.9	1893	H	US-08-188-582-11	11,
4	106	0.9	1893	Н	US-08-646-715-11	Sequence 11, Appl
S	95	5.4	2938	Ŋ	PCT-US94-00198-3	Sequence 3, Appli
Q	95	5.4	3969	4	US-08-061-376-5	Sequence 5, Appli
7	94	5.4	623	4	US-09-104-068-4	Sequence 4, Appli
8	94	5.4	637	4	US-09-104-068-2	Sequence 2, Appli
6	87.5	5.0	1704	4	US-08-485-355B-40	40,
10	84.5	4.8	1182	4	US-09-287-354-6	9
11	81.5	4.6	504	-	US-07-932-915-2	2,
12	81.5	4.6	504	Ŋ	PCT-US91-05826-2	Sequence 2, Appli
13	81.5	4.6	1207	4	US-09-287-354-5	5
14	81.5	4.6	1481	4	US-09-251-645-14	Sequence 14, Appl
15	80.5	4.6	1863	~	US-08-603-753D-2	Sequence 2, Appli
16	80.5	4.6	1863	4	US-09-099-753-2	Sequence 2, Appli
17	80.5	4.6	1863	4	US-08-986-106-2	Sequence 2, Appli
18	80.5	4.6		4	US-09-007-678B-49	49,
19	80	4.6	1142	7	US-08-993-118-7	Sequence 7, Appli
20	80	4.6		m	US-08-845-528C-7	
21	80	4.6		4	US-09-061-709-2	7
22	79	4.5		4	US-08-506-296B-56	é
23	79	4.5		4	US-08-506-296B-68	Sequence 68, Appl
24	79	4.5		4	US-08-506-296B-14	Sequence 14, Appl
25	79	4.5	2183	٣	US-08-746-111-5	2
56	79	4.5	3898	4		∢
27	79	4.5	4654	4	US-08-476-515A-84	Sequence 84, Appl

4, App.	6, App.	8, App.	0, Appl	a,			19, Appl		0, Appl					22, Appl			24, App.	
Sednence 8	Sednence 8	Sednence 8	Sednence 9	Sequence 8	Sequence 1	Sequence 1	Sequence 1	Sequence 1	Sequence 2	Sequence 2	Sednence 2	Sequence 2	Sequence 2	Seguence 2	Sequence 2	Sequence 2	Sequence 2	
US-08-652-877-84	US-08-652-877-86	US-08-652-877-88	US-08-652-877-90	US-09-032-523-8	US-09-012-710-12	US-09-556-273-12	US-08-425-061-19	US-08-825-886-19	US-08-425-061-20	US-08-825-886-20	US-08-425-061-21	US-08-825-886-21	US-08-425-061-22	US-08-825-886-22	US-08-425-061-23	US-08-825-886-23	US-08-425-061-24	
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79	79	79	79	78.5	78	78	77.5	77.5	77.5	77.5	77.5	77.5	77.5	77.5	77.5	77.5	77.5	
28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	

## ALIGNMENTS

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SEGULT 1
US-08-188-582-14
Sequence 14. 54 Application US/08188582
Sequence 14. 54 Application US/08188582
Sequence 14. 54 Application US/08188582
Sequence 14. 1870WA7110N;
GENERAL INFORMATION:
APPLICANT: D'AID APPLICANT: RUPPET 'Siegfried APPLICANT: Siegfried APPLICANT: Release #1.0, Version #1.25
COMMUTER: Siegfried APPLICANT: S
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285 LSQLTKID----GSLGPKESQSYGEGSSESLLTDIGI 317
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 11, Application US/08188582
Patent No. 5534410
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dynlact, Brian D.
Hoey, Timothy
Ruppert, Siegfried
Tanese, Naoko
        TELEPAONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELES: 910 277299
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 1872 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tjian, Robert
Comai, Lucio
                                                                                                                                         STRANDEDNESS: single
                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-646-715-14
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COMPUTER READABLE FORM:
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California
                                                                                                                             amino acid
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STATE:
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                                                                                                      1383 VTLSSILESIINDMRDLPNTYPFHTPVNAKV-VKDYYKIITRPMDLQT-LREN----- 1433
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1510 ILDNIVTQKMMAVPDSWPFHHPVNKKFVPDXYKVIVNPMDLETIRKNISKHKYQSRESFL 1569
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                                                                                                                                                       51 VLIQV------DLNKCEPWDIPKMACVGGKDWYFFYSQRDRKYATGLRTNRATATGY 100
                                                                                                                                                                                                                                      101 WKATGKDRTILRKGKLVGMRKTLVFYQGRAPRGRKTDNVMHEFR------LQGSHHPP 152
                                                                                                                                                                                                                                                                                                                                                                                                ---HHYIINEHVPCFSNLSQN ---- QTLNSNLT ----- 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         242 ---NSVSELKIPCKNPNPLFTGGSAS-----ATLTGLD-----SFCSSDQMVLRAL 284
                                                                           1 METEEEMKESS--ISMVEAKLPP-----GFRFHPKDDELVCDYLMR--RSLHNNHRPPL 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: RUPPERT, SIGGITIED
APPLICANT: Tanese, Nacko
APPLICANT: Wang, Edith
APPLICANT: Weinzierl, Robert O.J.
TITLE OF INVENTION: TATA-BINDING PROFEIN ESSOCIATED FACTORS,
NUMBER OF SEQUENCES: 36
                                                                                                                                                                                                                                                                                                                    153 NHSLSSPKEDWV-LCRVFHKNTEGVICRDNMGSCFDETASASLPPLMDPYINFDQEPSSY
Similarity 19.9%; Score 106; D3 1; Length 1872; Similarity 19.9%; Pred. No. 0.057; 9; Conservative 51; Mismatches 125; Indels 142;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/646,715
FILING DATE: U9-MAY-1996
CLASSIFICATION: 435
RIOR APPLICATION NUMBER: US 08/188,582
FILING DATE: 28-JAN-1994
ATTORNEY/ARENT INFORMATION:
NAME: OCCURED BATCHER OF US 08/188,582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ::| :| :| | | : | :| 1829 - AELESLDPMTPGPYTPQPPDLYDTNTSLSMSRDASV 1664
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: A-57650-2/AJT/RAO TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC_DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 14, Application US/08646715 Patent No. 5637686
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Comai, Lucio
Dynlact, Brian D.
Hoey, Timothy
Ruppert, Siegfried
Tanese, Naoko
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REGISTRATION NUMBER: 36,627
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APPLICANT: Tjian,
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                                                                                                                                                                                                              1330 IESADEVRRKSLVLKFPKQQLPPKKKRRVGTTVH------CDYLNRPHKSIHRRRTDPM 1382
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1570 DDVNLILANSVKYNGPESQYTKTAQEIVNVCYQTLTEYDEHLTQLEKDICTAKEAALEE- 1628
                                                                                                                                                                                                                                                                                              51 VLIQV------DLNKCEPWDIPKMACVGGKDWYFYSQRDRKYATGLRTNRATATGY 100
                                                                                                                                                                                                                                                                                                                                                                                                                                               101 WKAIGKDRTILRKGKLVGMRKTLVFYQGRAPRGRKTDWVMHEFR------LQGSHHPP 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             153 NHSLSSPKEDWV-LCRVFHKNTEGVICRDNMGSCFDETASASLPPLMDPYINFDQEPSSY 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          242 ---NSVSELKIPCKNPNPLFTGGSAS-----ATLTGLD-----SFCSSDQMVLRAL 284
                                                                                                                                                     1 METEEEMKESS--ISMVEAKLPP-----GFRFHPKDDELVCDYLMR--RSLHNNHRPPL 50
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APPLICANT: Tanese, Nacko
APPLICANT: Wang, Edith
APPLICANT: Weinzierl, Robert O.J.
TITLE OF INVENTION: TATA-BINDING PROTEIN ASSOCIATED FACTORS,
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING TAFS AND METHODS OF USE
NUMBER OF SEQUENCES: 36
Query Match 6.0%; Score 106; DB 1; Length 1872; Best Local Similarity 19.9%; Pred. No. 0.057; Matches 79; Conservative 51; Mismatches 125; Indels 142;
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ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT STREET: 4 Embarcadero Center, Suite 3400
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APPLICANT: Schering Corp.
TITLE OF INVENTION: RAS Associated GAP Proteins
                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                     San Francisco
                                           California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
                                                                                94111-4187
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PCT-US94-00198-3
                                                             COUNTRY:
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                     CITY:
STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1351 IESADEVRRKSLVLKFPKQQLPPKKKRRVGTTVH-----CDYLNRPHKSIHRRRTDPM 1403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1404 VTLSSILESIINDMRDLPNTYPFHTPVNAKV-VKDYYKIITRPMDLQT-LREN----- 1454
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   101 WKATGKDRTILRKGKLVGMRKTLVFYQGRAPRGRKTDWVMHEFR------LQGSHHPP 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      242 ---NSVSELKIPCKNPNPLFTGGSAS-----ATLTGLD-----SFCSSDQMVLRAL 284
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Wang, Edith
PEPLICANT: Wang, Edith
TITLE OF INVENTION: TATA-BINDING PROTEIN ASSOCIATED FACTORS,
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING TAFS AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      153 NHSLSSPKEDWV-LCRVFHKNTEGVICRDNMGSCFDETASASLPPLMDPYINFDQEPSSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                               6.0%; Score 106; DB 1; Length 1893;
19.9%; Pred. No. 0.058;
tive 51; Mismatches 125; Indels 142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
(SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/188,582
                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Osman, Richard A
REGISTRATION NUMBER: 36,627
REEFENENCE/DOCKET NUMBER: A-57650-2/AJT/RAO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 398-3249
TELEFX: 910 277299
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LEMETH: 1893 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1650 -AELESLDPMTPGPYTPQPPDLYDTNTSLSMSRDASV 1685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      285 LSQLTKID----GSLGPKESQSYGEGSSESLLTDIGI 317
                   CLASSIFICATION: 435
TORNEY/AGENT TWO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 11, Application US/08646715
Patent No. 5637686
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Tjian, Robert
APPLICANT: Comai, Lucio
APPLICANT: Dynlact, Brian D.
APPLICANT: Hoey, Timothy
APPLICANT: Ruppert, Stegfried
APPLICANT: Tanese, Naoko
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 19.9%
Matches 79; Conservative
                                                                                                                                                                                                                                                                                                                                                                            ; MOLECULE TYPE: protein US-08-188-582-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
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1484 KHSLIQISQSMLDLCDEKLKEKEDKLAR------LEKAINPLLD---DDDQVAFSF 1530
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           242 ---NSVSELKIPCKNPNPLFTGGSAS-----ATLTGLD-----SFCSSDQMVLRAL 284
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6.0%; Score 106; DB 1; Length 1893;
19.9%; Pred. No. 0.058;
tive 51; Mismatches 125; Indels 142;
                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
CURLICATION NUMBER: US/08/646,715
FILING DATE: 09-MAY-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: A-57650-2/AJT/RAO TELECOMMUNICATION INFORMATION:
TELEPAX: (415) 398-3249
TELEFAX: (415) 398-3249
TELEFAX: 910 277299
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
4 Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 09-MAY-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/188,582
FILING DATE: 28-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3, Application PC/TUS9400198 GENERAL INFORMATION:
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amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 6.0%
Best Local Similarity 19.9%
Matches 79; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; MOLECULE TYPE: protein US-08-646-715-11
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21;

Gaps

us-09-889-926-2.rai

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APPLICANT: Parry, Pauline
TITLE OF INVENTION: CHARACTERIZATION OF A CHROMOSOME 11Q23
TITLE OF INVENTION: TRANSLOCATION BREAKPOINT ASSOCIATED WITH ACUTE LEUKEMIAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2093 TIAHSPTSFTESSSKES-----ONTAELISPPSPDRPPHSQTSGSCYYHVIS-KVPR 2143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2144 IRTPSYSPTQRSPGCRPLPSAGSPTPTTHEIVTVGDPLLSSGLRSIGSRRHSTSSLSPQR 2203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    86 YATGLRINRATATGYWKATGKDRTILRKGKLVGMRKTLVFYQGRAPRGRKTDWVMHEFRL 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    146 QGSHHPPNHSLSSPKEDWVLCRVFHKNTEGVIC-----RDNMGSCFDETASASLPP 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    197 IMDP-YINFDQEP-----SSYLSDDHHYIINEHVPCFSNLSQNQTLNSNLTNSVSELK 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    249 IPCKNPNPLFTGG-----SASATLTGLDSFCSSDQMVLRAL----LSQLTKIDG 293
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11.1%; Pred. No. 2.5;
.ve 39; Mismatches 124; Indels
                                                                                                                                                                                                       E: Pretty, Schroeder, Brueggemann & Clark
444 South Flower Street, Suite 2000
                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/061,376
FILING DATE: 13-MAY-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 31,192
REFERENCE/DOCKET NUMBER: 941 9387
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619)546-4737
TELEPEAX: (619)546-9392
INFORMATION FOR SEQ. ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2264 NLQRTVVTVGNKNSHLDGSSSSE 2286
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; Patent No. 6238882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         294 SL-----GPKESQSYGEGSSE 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 13-MAY-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Relter, Stephen E.
REGISTRATION NUMBER: 31,1
     Evans, Glen A.
Djabali, Malek
Selleri, Licia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3969 amino acids
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; MOLECULE TYPE: protein
US-08-061-376-5
                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Pretty, S
                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                           CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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Best Local 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      110 YLTDKNLLAYLDILQHLSSYMK----RTIFHSLLYYASKAFLFWIMARPK----EYVK 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         198 FDDVYSTF--SGSSLLTNVNNDHHYHLHH-----SSSSSKTTNTNSPNSISKTSIKQSS 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    58 DLTIDYIQRFISASNH-----VEFTKCVKTKVVAPLLISHTSTELGVVNHLDLFGCE 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        140 MHEFRLQGSHHPPNHSLSSPKEDWVLCRVFHKNTEGVICRDNMGS-CFDETASASLPPLM 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         161 IYNNLISSDYNSPSSS------SDNGGSNNSDKTSISQLVSLL 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          199 -- DPYINFDQEPSSYL---SDDHHYIINEHVPCFSNLSQNQTLNSNLTNSVSELKIPCK- 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          253 -----NPNPLFTGGSASAT--LTGLDSFCSSDQMVLRALLSQLTKIDGSLGPKESQSY 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            250 VNASGNVSPSQFSTGNDASPTSPMASLSSPLNTN--ILGYPLSPITSTLGQANTSTST-- 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5.4%; Score 95; DB 5; Length 2938; 21.7%; Pred. No. 1.6; tive 46; Mismatches 121; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31 ELVCDYLMRRSLHNNHRPPLVLIQVDLNKCEPWDI ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTOKNEY AND ATTOKNEY AND ATTOKNEY AND ATTOKNEY AND ATTOKNEY BEGISTRATION NUMBER: 32,743
REFERENCE/DOCKET NUMBER: DX0352 PCT TELECOMMUNICATION INFORMATION: TELEFANNE: (201)822-7039
INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
LENGTH: 2938 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Saccharomyces cerevisiae PCT-US94-00198-3
                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: PCT/US94/00198
                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/004,824
FILING DATE: 15-JAN-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                              COMPUTER: Macintosh
OPERATING SYSTEM: 6.0.8
SOFTWARE: Microsoft Word 5.1a
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 5, Application US/08061376; Patent No. 6175000; GENERAL INFORMATION:
                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Schering Corp.
STREET: 1 Girald Farms
CITY: Madison
                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           306 ---TAATIKIDADIPSIM 320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein ORIGINAL SOURCE:
                                                                                                                                                                                                       COMPUTER READABLE FORM:
NUMBER OF SEQUENCES:
                                                                                                                               New Jersey
: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                        94304-1104
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                                                                                                                                                      COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      160 SG---SNHSLAS------INLADNLKELGLEIGRFKTGTPPRVKASSIN 199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66 YIQMKMLNTGKGPAVRALRAQADK-------ELYSKEMRKTV---ENQE 104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  147 GSHHPPNHSLSSPKEDWVLCRVFHKNTEGVICRDN---MGSCFDETASASLPPLMDPYIN 203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 5.4%; Score 94; DB 4; Length 623; Best Local Similarity 20.5%; Pred. No. 0.21; Matches 63; Conservative 50; Mismatches 103; Indels
                                                                                                                                                                                                                                                                   SEE: Dechert, Price & Rhoads
: 4000 Bell Atlantic Tower, 1717 Arch Stre
Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 19103-2793
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: PSASLENG for Windows Version 2.0b
CURRENY APPLICATION DATA:
APPLICATION NUMBER: US/09/104,068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUBBER: 60/051,379
FILING DATE: 01-UUL-1997
ATTORNEY/AGENT INFORMATION:
NAME: FEAL, Stephen T
REGISTRATION NUMBER: 36,795
REFERENCE/DOCKET NUMBER: 36,795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GM10029
                                                                                                                                    APPLICANT: Wang, Min
APPLICANT: Jaworski, Deborah D.
TITLE OF INVENTION: gidal
NUMBER OF SEQUENCES: 6
GENEFAL INFORMATION:
APPLICANT: Kallender, Howard
APPLICANT: Palmer, Leslie M.
APPLICANT: Fedon, Jason C.
APPLICANT: Lenox, Anna L.
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TELEPHONE: 215-994-2488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 623 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 215-994-2222
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US-09-104-068-4
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                                                                                                                                                                                                                                                                   ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36 YLMRRSLHNNHRPPLVLIQVDLNKCEPWDIPKMACVGGKDWYFYSQRDRKYATGLRTNRA 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5.4%; Score 94; DB 4; Length 637; 20.5%; Pred. No. 0.22; tive 50; Mismatches 103; Indels
                                                                                                                                                                                                                                                                            E: Dechert, Price & Rhoads
4000 Bell Atlantic Tower, 1717 Arch Stre
                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM Compatible OPERATING SYSTEM: Windows 95 SOFFWARE: FastSEQ for Windows Version 2.0b CURRENT APPLICATION DATA:
FILING DATE: US/09/104,068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: GM10029
                                                                               APPLICANT: Kallender, Howard
APPLICANT: Pelmer, Leslie M.
APPLICANT: Fedon, Jason C.
APPLICANT: Lenox, Anna L.
APPLICANT: Wang, Min
APPLICANT: Wang, Min
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/051,379
FILING DATE: 01-JUL-1997
ATTORNEY/AGENT INFORMATION:
NAME: Falk, Stephen T
REGISTRATION NUMBER: 36,795
               ; Sequence 2, Application US/09104068
; Patent No. 6238882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-994-2488
                                                                                                                                                                                                             TITLE OF INVENTION: 91dA1
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            637 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 20.59
Matches 63; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      215-994-2222
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COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                     Philadelphia
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                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                    USA
                                                                                                                                                                                                                                                                               ADDRESSEE:
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US-09-104-068-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
US-09-104-068-2
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                                                                                                                                                                                                                                                                                                                          CITY:
STATE:
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Qy 308 SESLITDI 315	:   :
:   16 STSLPEDV 323	QY 303 YGEGSSESLL 312
RESULT 9	Db 612 -GSGKTGTLI 620
US-08-485-355B-40 ; Sequence 40, Application US/0848535B ; Patent No. 6177075	RESULT 10 US-09-287-354-6
<pre>; GENERAL INFORMATION: ; APPLICANT: Christian, P. D., Gordon, K. H.J., Hanzlik, T. N. ; TITLE OF INVENTION: nasct viruses and Their Uses in</pre>	on US/09287
; NUMBER OF SEQUENCES: 57 ; CORRESPONDENCE ADDRESS:	; APPLICANT: THOMPSON, Catherine C. ; TITLE OF INVENTION: HUMAN HAIRLESS GE ; FILE REFERENCE: Thompson-20263/02443
; ADDRESSEE: Flehr Hohbach Test Albritton & Herbert LLP ; STREET: Four Embarcadero Center, Suite 3400 ; CITY: San Francisco	CURRENT APPLICATION NUMBER: US/09/287 CURRENT FILING DATE: 1999-04-07 EARLIER APPLICATION NUMBER: US 60/080
; STATE: California ; COUNTRY: United States	; EARLIER FILING DATE: 1998-04-07 ; NUMBER OF SEQ ID NOS: 10
; ZIP: 94111-4187 ; COMPUTER READABLE FORM:	; SOFTWARE: Patentin Ver. 2.0 ; SEQ ID NO 6
; MEDIUM TYPE: Floppy disk ; COMPUTER: 18M PC Compatible . ODPRDATING everew. Do-nog Medium	; LENGTH: 1182 ; TYPE: PRT
SOFTWARTING 3131EM: FC DOS/MG DOS ; SOFTWART Release #1.0, Version #1.30	; OKCANISM: MOUSE US-09-287-354-6
; CONTENT AFFILENTIAL ON MERRY (25/08/485,355B); FILING DATE: 07-Jun-1995	Chiery Match A 68. Conte
	Similarity 23.0%; 9; Conservative 16
	CGKI.VGMPKTI.VFVOGBADPGPI
~	
SPELICATION NUMBER: AU PL4081/92	-
	121
; REGISTRATION NUMBER: 31,801 ; REFERENCE/DOCKET NUMBER: A-58631-2/RFT/DSS	TONG
TELECOMMUNICATION INFORMATION:  TELEPHONE: (415) 781-1989	Db 168MSSLPPERPYDW
: TELEFAX: (415) 398-3249	QY 265 ATLTGLDSFCSSDQMVLRALLSQLTKIDGS
144	DD 198 AFGLGSKGFYHKDPNILRPAKEPLAE-SGM
TYPE: amino acids	Qy 307 SSESLL-TDIGIPSTV 321
COLOGICA: Ilnear  MOLECULE TYPE: protein  SEQUENCE DESCRIPTION: SEO ID NO: 40:	57 RQQNLCPVFLGYPDTV 272
•	RESULT 11
atch 5.0%; Score 87.5; JB 4; Length 170 cal Similarity 22.0%; Pred. No. 4.6;	US-7/-9325-913-2 Sequence 2, Application US/07932915 ; Patent No. 5672486
Matches 55; Conservative 35; Mismatches 73;	; GENERAL INFORMATION: ; APPLICANT: Soulillou, Jean-Paul
Qy 84 RKYAGERRYRATA TGYWKATGEDRTILRKGKLV3NRK TLYFYGGRAPRGRY 136	; TITLE OF INVENTION: Protein Polyli; TITLE OF INVENTION: Core; NUMBER OF SEQUENCES: 11
Qy 137 DWVMHEFRLQGSHHPPNHSLSSPKEDWVLCRVFHKNTEGVICRDNW 182  Ph 482 PRINTRY VALGROTT CONTROLL	CORRESPONDENCE ADDRESS:  ADDRESSEE: Cooley Godward Castro  STREET: S Palo Alto Square, Suit
183 GSCEPETAGAST. DPI MDY TNEHORDSCAYL SUDHHYTTNEHVDSGAN SONOFI NGNI SN	; STATE: California
532 AGCYNERPVPSTPPVEEPQGFDADLWHATAASLPEYRATLQAGLNT	COUNTAIN USA 1 ZIP: 94306 COMPUTER READABLE FORM:
	MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible

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84.5; DB 4; Length 1182;
No. 5.7;
smatches 92; Indels 89; Gaps 11;
|| : :: ||
TLSPVRGLEMYEGPP---- 611
                                                                                                                                                                                                                                                                                                                                                     I----- 151
                                                                                                                                                                                                                                                                                                                                                                    SRDNMGSCFDETASASLPPLMDPYINFDQEP 208
                                                                                                                                                                                                                                                                                                                                                                                                                                     SNLTNSVSELKIPCKNPNPLFTGGS----AS 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3L----GPKESQSYGE---G 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gands Joined To A Stable Protein
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35
17,354
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          76; Indels 89; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----DELVCDYLMRRSLHNN 45
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Best Local Similarity 21.4%; Pred. No. 12;
Matches 55; Conservative 22; Mismatches 91; Indels 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
4.6%; Score 81.5; DB 5; Length 504;
Best Local Similarity 22.2%; Pred. No. 3.4;
Matches 56; Conservative 31; Mismatches 76; Indels 8
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GENERAL INCORNATION:
APPLICANT: THOMPSON, Catherine C.
TITLE OF INVENTION: HUMAN HAIRLESS GENE AND PROTEIN
FILE REPERENCE: THOMPSON-20263/0243435
CURRENT APPLICATION NUMBER: US/09/287,354
CURRENT FILING DATE: 1999-04-07
EARLIER APPLICATION NUMBER: US 60/080,888
EARLIER FILING DATE: 1998-04-07
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PALENTIN Ver. 2.0
SEQ ID NO 5
                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/575,394
FILING DATE: 29-AUG-1990
ATTORNEY AGENT INFORMATION:
NAME: Rowland Ph.D., Bertram I.
REGISTRATION NUMBER: 20,015
REFERENCE/DOCKET NUMBER: FP55352-1/BIR
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-791-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 EEEMK -- ESSISMVEAKLPPGFRFHPKD-----
PCT/US91/05826
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                                                                                                                                                                                                                                                                                TELEFAX: 415-494-8771 INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 504 amino acids
TYPE: AMINO ACID
                     19910822
                                                                                                                                                                                                                                                                              415-494-8771
                                                                                                                                                                                                                                                                                                                                                                                                                    ; MOLECULE TYPE: protein PCT-US91-05826-2
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  APPLICATION NUMBER:
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                                           CLASSIFICATION:
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US-09-287-354-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        220 KESGPITYKVISTLIIKESDWLSQSMF-----TCRVDHRGLIFQQNASSMCVPDQDIA 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     128 -ADETATIVEFLNRWITFCQSIISTLTGSVIAELP---PKVSVFVPPRDGFFGNPRKSKL 183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80 EEELKPLEEVLNLAQSK---NFHLRPRDLISNINVIVLELKGSETTFMCEY----- 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Soulillou, Jean-Paul
TITLE OF INVENTION: Protein Polyligands Joined To A Stable Protein
TITLE OF INVENTION: Core
NUMBER OF SEQUENCES: I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match

4.6%; Score 81.5; DB 1; Length 504;
Best Local Similarity 22.2%; Pred. No. 3.4;
Matches 56; Conservative 31; Mismatches 76; Indels 8
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                             SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/932,915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Bertram I. Rowland, Ph.D. STREET: 4 Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 EEEMK -- ESSISMVEAKLPPGFRFHPKD------
                                                                                                                                                                                                                                                                                     NAME: Rowland Ph.D., Bertram I.
REGISTRATION UNDBER: 20,015
REFERENCE/DOCKET NUMBER: ATLA-001/01US
TELECOMMUNICATION INFORMATION:
                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US 07/646,875
FILING DATE: 28-JAN-1991
APPLICATION UNDRER: US 07/575,394
FILING DATE: 23-AUG-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application PC/TUS9105826
GENERAL INFORMATION:
         OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                               : 415-494-7622
415-857-0663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : 504 amino acids
amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , MOLECULE TYPE: protein US-07-932-915-2
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                                                                                                        FILING DATE:
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STATE:
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Sequence 14, Application US/09251645

Patent No. 6201413

GENERAL INFORMATION:
APPLICANT: Kramer, Vance C.
APPLICANT: Morgan, Michael K.
APPLICANT: Hart, Hope
APPLICANT: Hart, Hope
APPLICANT: Dunn, Martha
APPLICANT: Chen, Jang S.
APPLICANT: Chen, Jang S.
APPLICANT: Chen, Jang S.
APPLICANT: Chen, Jang S.
APPLICANT: OF INVENTION: NOVEL INSECTICIDAL TOXINS: FROM PHOTORHABDUS LUMINESCENS
TITLE OF INVENTION: NOVEL INSECTICIDAL TOXINS: FROM PHOTORHABDUS LUMINESCENS
TITLE OF INVENTION: NOVEL INSECTICANT: COG1963/A
CURRENT APPLICATION UNDRERS: US/09/251,645
CURRENT FILING DATE: 1999-02-17
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 14
LENGTH: 1481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23;
152 ---PNHSLSSPKEDWVLCRVFHKNTEGVICRDNMGSCFDETASASLPPLMDPYINFDQEP 208
                                                                                                                  147 PLIPEHSSGHPKSDPVAFRPLH-----CPFLLETKILERAPFWVPTCLPPYL---- 193
                                                                                                                                                                     209 SSYLSDDHHYIINEHVPCFSNLSQNQTLNSNLTNSVSELKIPCKNPNPLFTGGS----AS 264
                                                                                                                                                                                                                   194 ------PSPWVYSGSQPKVPS 223
                                                                                                                                                                                                                                                                 265 ATLTGLDSFCSSDQMVLRALLSQLTKIDGSL----305
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                                                                                                                                                                                                                                                                                                            224 AFSLGSKGFYHKDPNILRPAKEPLAASESGMLGLAPG3HLQQACDAEGPSLHQRDGETGA 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              980 FASSY--DDQQQLLRLTYQQSSWHHLIANELRVLGLPDGTRSDAFTYDAKHVPVDGLNLE 1037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     74 KDWYFYSQRDRKYATGL-RTNRATATGYWKA----TG--KDRTILRKGKLVGMRKT--- 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      923 ESRSYHYERIISDPQCNQDITLSSDLFGQPLKQ-VSVQYPRRNKPTTNPYP--DTLPDTL 979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                123 LVFYQGRAPRG------VRTDWVMHEFRLQGSHHPPNHSLSSPKEDW---V 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 865 NLYWLNRALKGOPLRSELYGLDGSAQQKIPYTVTESRPQVRQLQDNTTLSPVL--WASVV 922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  165 LCRVFHK-----NTEGVICRDNMGSCFDETASASLP----PLMDPYINFDQEP--- 208
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4.6%; Score 81.5; DB 4; Length 1481;
Best Local Similarity 22.5%; Pred. No. 16;
Matches 78; Conservative 33; Mismatches 90; Indels 145
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; ORGANISM: Photorhabdus luminescens
US-09-251-645-14
                                                                                                                                                                                                                                                                                                                                                                 306 GSSESLL-TDIGIPSTV 321
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US-09-251-645-14
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APPLICANT: ROBINSON-BENION, CHERYL L.
APPLICANT: THOMPSON, MARILYN E.
TITLE OF INVENTION: CHARACTERIZED BRCA1 AND BRCA2
TITLE OF INVENTION: PROTEINS AND SCREENING AND THERAPEUTIC METHODS BASED ON TITLE OF INVENTION: CHARACTERIZED BRCA1 AND BRCA2 PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE: adult
TISSUE TYPE: female breast
CELL TYPE: ductal carcinoma in situ, invasive
CELL TYPE: breast cancer and normal breast tissue
CELL LINE: not derived from a cell line
                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: ARLES A. TAYLOR, JR. STREET: SUITE 1401, UNIVERSITY TOWER, 3100 TOWER STREET: BOULEVARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 800 kB storage COMPUTER: IBM PC/XT/AT compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LIBRARY: CDNA library derived from human CLONE: Obtained using published sequence CHROMOSOME/SEGMENT: unknown MAP POSITION: unknown UNITS: unknown PEATURE: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: Windows 3.1 SOFTWARE: WORD PERFECT 6.1 and ASCII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/373,799
FILING DATE: 17 JAN 1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/603,753D
FILING DATE: 20 FEB 1996
CLASSIFICATION: 514
                     Sequence 2, Application US/08603753D Patent No. 5891857 GENERAL INFORMATION:
                                                                                                       APPLICANT: JENSEN, ROY A.
APPLICANT: PAGE, DAVID I.
APPLICANT: KING, MARY-CLAIRE
APPLICANT: SZABO, CSILLA I.
APPLICANT: JETTON, THOMAS L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: ARLES A. TAYLOR, JR. REGISTRATION NUMBER: 39,395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 12
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 493-8000
                                                                                         HOLT, JEFFREY T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (919) 419-0383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NORTH CAROLINA: USA
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                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein HYPOTHETICAL: no
                                                                                                                                                                                                                                                                      TITLE OF INVENTION: CITILE OF INVENTION: PITTLE OF INVENTION: CINUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                        DOULE CALY: DURHAM STATE: NOTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IMMEDIATE SOURCE:
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US-08-603-753D-2
                                                                                         APPLICANT:
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16;
NAME/KEY: BRCA1 protein
LOCATION: 1 to 1863
LOCATION: 1 to 1863
LDENTIFICATION METHOD: observation of mRNA and
LDENTIFICATION METHOD: antisense inhibition of BRCA1 gene
OTHER INFORMATION: regulatory effect on growth of human mammary cells.
OTHER INFORMATION:
AUTHORS: Miki, Y., et. al.
AUTHORS: Miki, Y., et. al.
TITLE: A strong candidate gene for the breast and
TITLE: ovarian cancer susceptibility gene BRCA1.
JOURNAL: Science
VOLUME: 266
PAGES: 66-71
DATE: 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          448 HSKSVESDIEDKIFGKTYRKKASLPNLSHVTENLI----IGAFVSEPQIIQERPLINK-L 502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 4.6%; Score 80.5; DB 2; Length 1863; Best Local Similarity 20.1%; Pred. No. 29; Matches 73; Conservative 49; Mismatches 152; Indels 89; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              293 TKDRMNVEKAEFCNKSKQPG-------LARSQHNRWAGSKETCNDRRTPSTE 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       53 IQVDLNK---CE--PWDIPKMACVGGKDWYFYSQRDRKYATGLRTNRA-TATGYW---- 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 338 KKVDLNADPLCERKEWNKQKLPC-----SENPRDTEDVPWITLNSSIQKVNEWFSRSD 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  102 -----KATGKDRTILRKGKLVGMRKTLVFYQGRAPRGRKTDWVM---HEFRLQGSHHP 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1: :: : | | : | | : | | 391 ELLGSDDSHDGESESNAKVADVLDVLNEVDEYSGSS---EKIDLLASDPHEALICKSDRV 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           152 PNHSLSSPKEDWVLCRVFHKN------TEGVICRDNMGSCFDETASASLPPLMDPYI 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   203 NFDQEPSSYLSDDHHY----IINEHVPCFSNLSQNQTLNS----NLTNSVSELKIPC--- 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            252 ---KNPNPLFTGGSASATLTGLDSFCSSDQMVLRALLSQLTKIDGSLGPKESQSYGEGSS 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              563 QNEKNPNPIESLEKESAFKTKAEPISSSISNEL----ELNIMHNSKAPKKNRLRRKSST 617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 TEEEMKESSISMVEAKLPPGFRFHPKDDELVCDYLMRRSLH------NNHRPPLVL 52
                                                                                                                                                                                                                                                                                                                                                                                 RELEVANT RESIDUES IN SEQ ID NO: 2: granin box RELEVANT RESIDUES IN SEQ ID NO: domain at amino acids 1214-1223 US-08-603-753D-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Search completed: July 15, 2002, 06:57:04 Job time: 136 sec
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